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(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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-1-

BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

-2-

RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

-3-

frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

-4-

SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

-5-

DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

-6-

polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

-7-

and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

-8-

conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

-9-

and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

-10-

samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.
10
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

-11-

sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

20 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

-12-

hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

-13-

sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

-14-

5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

-15-

A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with - polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

-16-

match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

15 $p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2$.

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($cum p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30

$$cum p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

-17-

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

-18-

incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

-19-

circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

-20-

(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

-21-

might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

-22-

D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

-23-

for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

-24-

Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

-25-

corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

-26-

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *5 Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

-27-

the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

-28-

100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

-29-

comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

-30-

corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

-31-

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
WI-7070	226	C	T	---	---	TGTGAACTCCACTTGAAGCCAAAGAAAGAACTACACCTAAACACACATGCCAGTTGGGAAGGCTCT GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAGAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTTTC/TJAGTTTAAATGCTGTGCTCTGTCTCAG
WI-10744	61	G	C	---	---	AAGCCATTGACGTAACTCTCAGAGGTTATTTGCATGGATTGACTCTCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTCGAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTT GATAATACATAAAGCCCTAGGATTTAGATACAATCTTGAAAGAACTGAGACAGATAATCTGAAATT AAATGAGGTAAGTTTTCAGGCACTCA
WI-9975	126	C	T	---	---	GGGCAATTACCAGCAAAAAGTCAAATACCAGCATCAAAGTCAGTGCAAAAGGAGGTAGAACAA TTACAGTAACATATGTCATCTTTTGTATATTAGTATTATCTGCCAATGCCGTAGAATA[C/T]JAGTG GGTCCCTAATAGTTATTAGTTCCCTTTTCTCTCTCTCTCTCAATCTCTGAAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAATGTAATGATCAATTTGATCTTACTGAA
WI-8010	247	G	T	---	---	GCTAGGTTTGTCTGTGGCTGCTTCACTAGACTTGAGATGACTTGATTTACAGTAATCCCTATGTT GATGTAACATAGCTAGACCTTCCCTTCTCGCAATTCAGCTCCAGTTTCAGAAAGTATGCCACAC TCAACCTTCTCTCCAGTTCATCCTGTATTAATTTCTCCCATATTAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAGAGATCCCCAAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G	C	---	---	GCCCGGCCTATCTTTAAATTTAACTTGATCTTTGGTGTCTCCATCTCTAGGATTCTGCCTTATAAT CTTTGTCTGTCTGTGTA[G/C]JATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTGCTATTGAGGACATTTCCACTTTCTACTTAA TCTCGACTCTATAACAACCTCCAACAGAA
WI-5222	52	G	C	---	---	GCCCGGCCTATCTTTAAATTTAACTTGATCTTTGGTGTCTCCATCTCTA[G/C]GATTCTGCCTTAT AATCTTTGTCTGTGTAGATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAATCTTCAGGTCTCTTTGAATTTTCTGCTATTGAGGACATTTCCACTTTCTACTTAA TCTCGACTCTATAACAACCTCCAACAGAA
WI-8007	242	C	A	---	---	TATGCACCTTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAAATGATAAAAATAA ATATGTTATTAGGCATTTATTACTAATACTAGTCCCTTCTTGGAAAGGAACACCCAAACCAATACTT ATAAGTACATGTAATTTATAGTAACATATTTACTATATACATATGGAAGAAATCATATTTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[C/A]JAGCTGCTG
WI-9823	97	C	T	---	---	TCAGTTGCCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTTTTGTTAG TCTATATTCACACATATGAGTGAAATTTTC/TJGGGCGCATGGGAAATACATCTTTATGAGACATTTGA ACTGCTCACCACCTATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTTAC ATGCTTTCCAATCTGATTTTGTATGACTATTGTATGCACAGTTGGATCACC

WI-9651b	105 A T ---	---	TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTCCT ACTTGCTCCTCATGTACAATTTTCTGCTGCTCTTCA/JATGGGCGAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGCGACTGCCAGGGACCCCTTATAGGCCTCTG TCTTTAAACCTGTATGGTATATTAAATCCCTGGTGTTTGAATGCTCTC
WI-9651	139 T C ---	---	TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTCCT ACTTGCTCCTCATGTACAATTTTCTGCTGCTCTTCAAGGGGAGCTTGCAAGCCTCCCTTTAGACACCT CT/JACAGGTACAGCCGACCATGCCCTACCTCCATGCGACTGCCAGGGACCCCTTATAGGCCTCTGT CTTTAAACCTGTATGGTATATTAAATCCCTGGTGTTTGAATGCTCTC
WI-7676b	309 A C ---	---	GTGACCTTCCTGCAGCGTGAGATGGCACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTTCTTGCTGCTGCTGGGTTCAGGGGCGAGGAGCGGTGGAGCTGCAGCTTCTGCTGGTGC TCCCCCGTCTCCTGGAGGCGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCCTGCAGCGTGAGATGGCACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GC/JTGGCTTCTTGCTGCTGCTGGGTTCAGGGGCGAGGAGCGGTGGAGCTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGGCGAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGCTTGGGCTGTGTTCAATTCATCTTCTCTCTCCATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGTAGTTTGAATAATTTTGTG/JATGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTGTTATAGGAGTTTGGCCATGACCCCTTTATGAGGAGAAAAAGGA TGACCCCTTTTGGCTCTACAACCTTATAGATAATTTAAATATCTTT
WI-9986	42 T C ---	---	TTGGTGTGAACCTCAGAAATATAGGGAAAAATAGACAATTTGAAT/A,CJGTACCCCGAGGAAACAAGAG CCCTGCACCTGACTCCAAAAGGAGTTCTATTATCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACCTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTCCCACTCTCATCAGGCCAAGTGGAGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCTTCAGAGAGCTGAAAAGGGTCCCTCGGGTCTTTTATTT CAGGGCTTGCATGGCTCTATTCCCCCTCTGCCCTCTC/JCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAGCTCATTTGTACAGTGTCTTTCATGTAATAA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGATACCCCAACTCACTAATTTAATCACTTATGTGCTATCAGATATCCTCTCT ACCTCAGCTTATTTGAAGAAAAATCCTAAACATCAAAATACCTTCATCCATAAAATGTGAGCATTT /CJATTAATAAACAAATAACTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	---	TCCTATTGCAATTCACAGTAGCCCCCATGAAGTAGGTATAACACAGCCTCTATTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAATAAGCAAGACCTGCA/AC JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTTGCTGTCAGCCAGGACCCCATGCGCA GAAAGCCCGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACCTTTGGAGATTCAATTTCTTGAGTGGCACTGCAT GCTCAATTCAGTGAAGAACTTGTGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGACTTTGG/GA/CTCCAGACTTCACTGTCTTAGGCATTGAACCATCACCTGGTTTGCACTTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	---	AAACACACAGAAATCATCAAGCAC/ATATCTGTGTTTGAGATAAATGATGCTGAGTCACCTATG TAAGAAGTAACCTGAAATAGTAGGATAGTATTATCAATTTCTGTAAATAGATTCACCTCTCAGCAAT TGGTCTGTTTCACTCTATGGAACCTCTCGTACTGTAATTTTCAATCTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTGTCC TTTCAATAAAGAGATGACATGATTGAACATGTGTTTAGATAAAGGGCACCTT/GTJGCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 T G ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTCTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTT/GJACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTTCATTCAACAATTCGTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGCTAGTGTCTTGGGTGTGAGCGGATT AT/GAJCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTTCATTCAACAATTCGTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCGCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	---	TCAACACGCTTTTATGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCTCTGACACTGCGCAAGT TAAAGAAAAACCTGCTTGTGTGAGAGGGAGGGCCAGACAGGGAGGAATTCAGGGGCATGTATGGCTC AGTCCCCTCT/GJ/ACTGCAGAGTATAGGGACCAGGGTTCCTCAAACTTT
WI-9484	178 G A ---	---	---	TCAACACGCTTTTATGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCTCTGACACTGCGCAAGT TAAAGAAAAACCTGCTTGTGTGAGAGGGAGGGCCAGACAGG/GAJAGGAATTCAGGGGCATGTATG GCTCAGTCCCCTCTGACTGCAGAGTATAGGGACCAGGGTTCCTCAAACTTT

WI-7330	207	C T	---			AGGATGGAAGGAGACACGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTTTTAAATGTGGCATATAGGTTT GTGACACAAGAAGTCATACCTTTGGTGGCTAAGTTTACTAAGGAAATAAATGAAAGATTAAAG TGAGAG[C/TTGAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
WI-9443	211	G A	---			TTAAACAGTTACAGTTGGTGAAGCAGAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACIT GCACAAATTAATCCTTTGGATCATACAACTGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACTCATGGAAGGAGTCTAGAGTCCATCAGCTCAGACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCCACATGCCACIT
WI-7166	59	C T	---			TCTCTAAAGAGAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/TTGGAT CATCAACAAGATTTCCTTGTGCAAAATATTTGACTATTCTGTATCTTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTAACTTGTGCTGTGAACAAATGTCGAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189	T C	---			GCTTCTTCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGCGGGAGCAATTTAGCC CCACCTGTCTCCATCTGCCCCCTGCAACAGCTGAGGCTGCTTCTCTCTGAGTTCTCTGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[C/TTGGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTGAGGGGCCCCAACITCCCTGGAGCTC
WI-7259	188	G T	---		C	GCTTCTTCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGCGGGAGCAATTTAGCC CCACCTGTCTCCATCTGCCCCCTGCAACAGCTGAGGCTGCTTCTCTCTGAGTTCTCTGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[C/TTGGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTGAGGGGCCCCAACITCCCTGGAGC
WI-7322	275	A G	---			GTACTTTAGGCCTGTGAGGGTGGCAATTTAGTGTGACCCCTTGACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCTATATG GCCATAAAGTGCCTAAGCACTCAGGCCCTCCCACTCATCAACCCCTTTGACCCAGAGAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGGCCTCTGGCTG
WI-7685	46	T C	---			TCAGTTCTAGTCTCTTGGGGCCACACAGAACTCTTTTGGGCT[C/TTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGCTTTGGAGCTGAGCCTCTCACCTGTACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCTCCCTCTGCGGACTC CTGGGTTGAGCTGTTGCCTCAGTCCCCCAACAGATGCTTTCTGTCTC
WI-563	87	G A	---			TGTGACCAATTGTTATTTAGAGGGTTTAACAATGGCCTGACTATCACCTGATGGTCGCCAGAAATTC CTGGGGAGGGCCTCCCT[G/A]CCCTGATCATGTCTACCTAACCTGCTACTCTAACATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAAAATTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191	C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTCTGTGTGTCAAAATGATCCTTCT GTTGCTGCACTGTCTACTTGTGTATGGATTATAATTATGTCCAAAAAAGCC[C]A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-931b	81	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTA/G]TCCCTCACCACACCTTCCAGTGTCTTCTGTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTACTTGTGTATGGATTATAATTATGTCCAAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-931	31	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGTCTTCTGTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTACTTGTGTATGGATTATAATTATGTCCAAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTGAGA
WI-10870b	91	CT ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAAGTGGG[C]T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGATACAAAATAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATACGTTGCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAAGTGGGACCTACTTAGA[G]A]CAGTGGAGTACCCCTGAGTACGACCCCC TAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGATACAAAATAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATACGTTGCCCCC
WI-7719b	281	T C ---	---	AGTTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCAGTATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTGGGCATTGGTCTGGCCAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TCTTAGTGAAGACAATGTACAGTTATCC[G]T]TAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCAGTATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C]A]GTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTCTTTTGTGA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTCAAG TTAACAGCCACCATTGTGTAACACTTTGT

WI-10673	94 C G ---	---	TCCCTTATGACCCCAAGAGATAATTTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/GT]GCAGTTGGAACATATGCAGTGTCTCCGGCCACACA TCTGTCTGGGCCCCCTACCTGCCCAATTCATCTGCAATAACTCTGCTTATTTGTTTCATCCTG GAGAAITGAAGGGAGGTCAAGTTGTTGTCAATGATTTGTGAGAGAACCT
WI-7842	57 T C ---	---	CACAGCCATGCCCTTGAGGAGCGGCCACACAGATGCTGAATCCCCTATCCCATTCTG[C/G]GATGAG TCCCAATTCGCTTGCATTTAGCAATCTGTCTCCCCCAAAAAGAAATGTGCTATGAAGCTTTCTTCT ACACACTGTAGTCTCTGAATGAAGCTGAAGGCTTAGTACCAGAGCTAGTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	CTGCCCTCATCAGCCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCACCCAGCTGTACCCAGCCCGGGCAGGTGCAGCCCTTCTCTCC TGCTCTG[C/A/C]TCTGACTCTCTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCTCTTACTGGGGCTGGGGCTCTAGCCCCA
WI-4767b	173 C A ---	---	TTCCAGTCTGTTTATCCCTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGAC[C/A]AAATCACTAAGGAAATCCACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---	---	TTCCAGTCTGTTTATCCCTTTCATTGTCAAAAAGATGCTCTTAGACTG[A/G]ATTCATAAAGAGTT CCTCAGGTCTGGTAACTCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTGGAGAGGGTATG TTTCTGCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAAATCCACTAAGAC TCCCTTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAT
WI-7718e	60 T C ---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718d	31 G A ---	---	ATTGCACTGAAGTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT

WI-7718c	91 C G ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248 A G ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42 A T ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTC AAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT
WI-7227d	99 G C ---	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTTAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAATG
WI-7227c	291 G A ---	---	---	AGGGAATTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227b	93 G T ---	---	---	AGGGAATTGTTGCTCCTGGAGG[A/G]AGCCCCAGGCATCATTAAACAAGCCAGTAGGTACCTGGC TTCCGTGGACCAATTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	---	CCACAATGCCTCTCCACGATGTCAGGACTCCTGTCTGCTCTGGAGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCATGTTGATCCTTCATCGAACAACTGATGCGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAATGAGCCAAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCTCCCATCCCA[A/C]ATGATCTTGAGATTTC
WI-7310b	234 A C ---	---	---	

WI-7310a	64 T A ---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGGAGACAAGGAACCTT/A JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGATCCTTCATCGAACAACTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAAGACATGTCTATTGAACCTGAGGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCATCCCAATGATCTTGAGATTC
WI-7878b	162 A G ---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGACTCCTATGATGGCTGTGGTTGATAATAATCA GATCATGCCCAAGACGGCCCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGCAATGCGTCC CTGAGGAGAAATCTGGAGGAGCTG[A/G]GTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTGT CTGTGGGAGCCAGGAAGCTGCTCACCAAGATTGGTGCAGGAAACTA
WI-7878a	51 C G ---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGACTCCTATGATGGCTG[C/G]TGGTTGATAATAA TCAGATCATGCCAAGACGGCCCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAATGC GTCCCTGAGGAGAAATCTGGAGGAGCTGAGTGTGATGAAGTGTATGTTGGAGGGAGCACAGTG TCTGTGGGAGCCAGGAAGCTGCTCACCAAGATTGGTGCAGGAAACTA
WI-7381c	213 C T ---	---	CTCCACATTCACACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGCAGGAGCAGGCTGCAGGTTCTCTGCCTATGTTGAGATC AGATGTGCCAAGGAAGAGCTCTGGTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTC[C/T]GGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATTCACACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCC[C/G]CTTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGCAGGAGCAGGCTGCAGGTTCTCTGCCTATGTTGAG ATCAGATGTGCCAAGGAAGAGCTCTGGTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATTCACACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCC[C/G]CTTTCTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGCAGGAGCAGGCTGCAGGTTCTCTGCCTATGTTGAG ATCAGATGTGCCAAGGAAGAGCTCTGGTCCAGAGAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTCCGACCCCTCATATTAAATAGAGCAATGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAA[G/A]GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTCCGACCCCTCATATTAAATAGAGCAATGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAA[G/A]GGATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC

WI-1795b	130	T C	---			GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTCTTCCAGACTCCTACGATTAAATTGTATGCTGAACAACCTGATGAGTACTTAGATCTCAGTCTTGCAGAAAGAAAGT/CJC GTCTACCATTTTACCAAAATTCGTAGTACAATTAAGTATCTCTGTATCTCCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47	T C	---			GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGT/CJC TCCAGACTCCTACGAT TAAATTGTATGCTGTAACAACCTGATGAGGTACTTAGATCTCAGTCTTGCAGAAAGAAAGTCTC GTCTACCATTTTACCAAAATTCGTAGTACAATTAAGTATCTCTGTATCTCCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136	G A	---			CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGTCTCCTATCACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCAATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616c	136	G A	---			CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGTCTCCTATCACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCAATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616b	141	C T	---			CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGTCTCCTATCACATTGCCA CGTAGC/CJTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCAATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616a	116	G C	---			CACACAAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGTCTCCTATCACATTG CCACGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCAATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-1126c	52	G A	---			CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGCAAACTCCAGTATCAGT/GAJATACTAATAA AAACCTGTAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTTCAAGTTTCCCTCAAAAGGAATATGAAATT TGTTAAATGCAAAATCCAGCTGTAACTTTTTTGGACTTGCTTTATTTCTT
WI-1126b	230	T C	---			CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGCAAACTCCAGTATCAGTATCAGTATATAAAAA CCCTGTAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCGCAAGAAATTT TATTTCTCAAGATATAAAAAATAAATAATTTAATTTCAAGTTTCCCTCAAAAGGAATATGAAATTTGTT AAAATGCAAAATCCAGCTGTAACTTTTT/CJGGACTTGCTTTATTTCTT

WI-1126a	97 T C ---			CTCTATTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATATAATAAAAA CCCTGTAAGTCTGCTTGCAATTTTCAAGATTC/CAATATATATCCAGATTGTTTTCCAGCAAGAAA ATTTATTTCTCAAGATATAAAAAATAAATATTTAATTCAGTTTCCCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACTTTTTTGGACTTGICITTTATTTCTT
WI-11183c	124 C T ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACITTGAAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT TTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATAGGATAGAGTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACITTGAAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATAGGATAGAGTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAAACITTGAAAAATTTAGAGTAC ATATAAATAAATAAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT TTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGATAGGATAGAGTTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---			GCTTGGTTTGCTTTAGTCTTATTGCTCAGTCTTGAGTTCTCCCTTTCTGCTGGCCCTTTTGATTT CCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGGCTCTTCCCTTGACTTTCTC TTCACCAACCTTCTTTTATTTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-10770a	49 G T ---			GCTTGGTTTGCTTTAGTCTTATTGCTCAGTCTTGAGTTCTCCCTTTCTGCTGGCCCTTTTGATTT TCACCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGGCTCTTCCCTTGACTTTCTC CTGTTACCAACCTTCTTTTATTTCTTCAGGACACTCAGTTACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-9667b	82 C T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCTGTATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTAACCCAGTACCTAAGTCCAAACTTGCATTTCT
WI-9667a	68 G C ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCTGTATCATG G/C]TTATCACTGGACACAGCCACCTCCCGCAGGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTAACCCAGTACCTAAGTCCAAACTTGCATTTCT

WI-10400d	189 A G ---	---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAGAAAGTAATTGCAATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCAGTGCCATGTAG TTTTTGGTTCAATTTACTTGCAAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---	---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAGAAAGTAATTGCAATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCAATTTACTTGCAAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---	---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAGAAAGTAATTGCAATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCAATTTACTTGCAAATTTATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---	---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAGAAAGTAATTGCAATTTTCAGACATCT GCTGGTTAACTGTTATAAGATGTTTAGCACACATGTAAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTCCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCAATTTACTTGCAAATTTATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---	---	AAAGGGCTACAAACTAAGGCCAAACCAATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCAAC/TTTAGAAAGGGCATTCAAGCACATTCATGAGGCTTCATATACTGTTAG CAAAACAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTCCCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGACACATGACATAGGCTTAA
WI-10809a	33 C T ---	---	AAAGGGCTACAAACTAAGGCCAAACCAATGAAC/TTGGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCACCTTAGAAAGGGCATTTCAGCACATTCATGAGGCTTCATATACTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTCCCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGACACATGACATAGGCTTAA
WI-7038c	266 T C ---	---	CGAGCTTGGGATAAGCAAGGGACCTTGGGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGAAAGACTGTGAGGAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAAGATCCTGCAATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---	---	CGAGCTTGGGATAAGCAAGGGGACCTTGGGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCAGCCTGGCCAGAC AAGAA/CTGACTGTGAGGAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAAGATCCTGCAATTTATGGTGTAGTTCTGTA

WI-7038a	31	G A	---	---	CGAGCTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATACTAGATGCTGGGCTGCTCCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCA GACAAGAAAGACTGTCAGGAAGGGTCGGAGTCTGTAACACAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTCTGTCTGCCACAGTGAACCAAGCAGCCAGGTGCCAGGGTCCGAGGTCCACACA[G/T] CCCTCAGCCCCCTCAGCTTTGCAATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATTCCCAAGTCTCCTCCTCTGATTTGGATCTAGCAAGACCAGACGCGTCCCTAGAA TCCTGACTGTAAACAAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTCTGTCTGCCACAGTGAACCAAGCAGCCAGGTGCCAGGGTCCGAGGTCCACACA[C/T]AG CCCTCAGCCCCCTCAGCTTTGCAATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAAATACAGATTCCCAAGTCTCCTCCTCTGATTTGGATCTAGCAAGACCAGACGCGTCCCTAGAA TCCTGACTGTAAACAAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTGAGCCCCATTCT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAA[G/T]GGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAA[G/T]GGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCAT
WI-6711b	226	G T	---	---	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAATTTGAATAAGTATTTGGGAAGAAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTCACTGAAAT TTCATATACCTCCATTATTAAATTCATATACATCATTTGCAGAGAAAAGACAAACGGTGCCAACTGGGT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C	---	---	GGCTATTTGTAAATGCTTGGTTATTTGACTCCAAAATTTGAATAAGTATTTGGGAAGAAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAACTCACTCT GAATTCATATACCTCCATTATTAAATTCATATACATCATTTGCAGAGAAAAGACAAACGGTGCCAACTG GGTTTGGTGGTGCCTGCACACCCACAGTGGCACTAAGTGAATCTCTAAA

WI-10613b	172 A C ---			ATTGTATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTG/C/GCCCCAGGAGGTTACTATAATTTAGA AAGGCTCTACCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---			ATTGTATGCCAAATCATAATACCCCTGCATTCTAGAAACATACA[G/A]GTGTAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTACCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA[A/ TJGGAATGAACCACTCCCTGCCATTCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A ---			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGAAGC ACATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T ---			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTGCTTTCCAACAAGTGACTACCCCTTGA AGCACAATCCCTCTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAATATCCCAAGACCCAGGCAATTTTGCCCTCT TCCACATGCCCCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A ---			ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC[T/A]AAAGACAGCCATTTTAACTTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAGGAGGAGTGACGCTCTGTTAAAG
WI-10681a	41 A T ---			ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTGACTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCCCTAAAGACAGCCATTTTAACTTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAGGAGGAGTGACGCTCTGTTAAAG
WI-7222c	126 G T ---			GCCTCTCCTCAACTGTCCTGGACCAAGGCTAGGAAAGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG[G/T]AATAA AGGAGGGGAATTCCTTTGAACAAGAACTGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAGGTTGATTTTCAAGACTCGAATTCATTTT

WI-7222b	255	G A ---	---	---	GCCTCTCCTCAACTGCTCTGGACCCCAAGGCTAGGAAGGGCTGCTGAGATGACTGTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCAACCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G T ---	---	---	GCCTCTCCTCAACTGCTCTGGACCCCAAGGCTAGGAAGGGCTGCTGAGATGACTGTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCAACCCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A ---	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTC[A/ATTATCTCTCCAGTTCAAATG CTTGCACTCTTTAATAGCCAGCACTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCT TCTGTGATAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGGCCCTT
WI-8054c	237	G T ---	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCACTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCAAA TCTCTTTGTAGTTTAGCCCTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCTCC TGTCATAACGCCGCTTCCCTGGCGGTACAGA[G/TAATCCTTGGCCCTT
WI-8054b	148	T C ---	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCACTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCAAA TCTCTTTGTAGT[C/TTTAGCCCTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCT TCTGTGATAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGGCCCTT
WI-8054a	131	C G ---	---	---	AAAGATGACACTTAGAACTGGATCAGTTGGCCCTTCTCTTCTTATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCACTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAG[C/GJA CAATCTCTTTGTAGTTTAGCCCTTTCCGGAAATCGGCTTAGTTGGCCACCATAGCCACTCTGCT TCTGTGATAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGGCCCTT
WI-10854b	152	G T ---	---	---	TTCCACAAAAACTTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAAACACGAGACGATAGTTAACGCTCTGGTAAGTTAT ACGGTGTGCGAGGCAACA[G/TTGGAGAGGTACGGGAATAGTTCTACTTCCCTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T ---	---	---	TTCCACAAAAACTTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAGCGAAGTTGAAACA[C/TTGAAGACGATAGTTAACGCTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCCCTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A ---	---	---	AATTTTATATGGAAGGTTAGCAAACTATGCCCCACAGGCCATTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTGTTTGCACGCAGTTGAGCCATTGTGACAGAGGCTGTATG/AGCCTT CAAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAAGTGTGAA
WI-9826	125	A T ---	---	---	AATTTATATGGAAGGTTAGCAAACTATGCCCCACAGGCCATTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTGTTTGCACGCAGTTGAGCCATTGTGACAGAGGCTGT/ATJGGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAAGTGTGAA
WI-15986	60	T G	TTGTTTGTGT GTGGGTTTT	TGACATTATAT AAACGTAAAA GAAATGT	CGGACACGTTATATACAAATACAGATCGTATGGGTTTGTGTGGGTTTTTTTTT/GJTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G A G	AACTGCAAAAT AGGAAACCCAG	CCACCTGGGGC TCCC	TTCAAGTAAGTCAAATAGGAAACAGAG/AGJGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGAGGAGGTGGCCCCCTACACCCTTTAT
WI-8170b	259	G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTTCTCTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGAGAGATTACAAGGTTAAGATCATGTGTCATCAAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAAGGGCCCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTTCTCTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTGGTGAGAGATTACAAGGTTAAGATCATGTGTCATCAAAAGTGCAATCCTATCAATCAGAA A/T/AAAGGTAAAAGGGCCCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136	C G A C A	CCTTTATTAAA ATTGTTTCTT GACA	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCCATTAAACAAGCTTTTAAATCCTTCGGTAACTCCCTTTATTAATAATGTTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTCTCTCCACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAATTTCTGT	TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAAATTGATCCCTTATTTTACATGAAATAAAAACAATTTCTGTTGC/G/AGCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCCTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAAACCAAGCATGGGATTTTGCCGGAAAT ATTAGCGTTAAAGGAG/C/TTGAGTTGAGTCAAAACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG/G/AGAGATGGTCAGGCTTCTCTG TTCTTAACCCAGCAGAGCCCCAGCAACCTAGAAAGCGCCTCACCTAGCCTCTTAAT

WI-8827	22	C T	TOCCCTGGAG T TACTATGG	GC GATTAGGAT T TTAGTGTTCA C	GGTGCCCTGGGAGACTATGG[C/T]AGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTTCCTTCTATCCACCCAGCTTCT
WI-8833	51	A T	TCTCCATGCC T ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTTTAAAGCTCTCTGTAGACTGTCTTCCATGCCATTCTCTG[A/T]TGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63	A G	---	---	ATTTTTAGCCATGTTGGTAAAGTTCATTTTAGTACATGGTAAACCCAGGCCCTTCCCT[A/G]T TATATCCAGGTATGCTACAAGTTCTTTAACTCTTATCAGAAGTTATTATTACTGTTCCTTAGAGAG GCTACCAAGGCTAAATTCACCTAGTTGGTTTGCTAATGTCTCATTTATTTATCCTGAAGCTCGTG
WI-8850	21	A G	GGGACTTAAC CTTTGGCCT	CAAAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A/G]CCTGCCGTGGTGTGGCTCTGCGCTGTCTTTTGGTTCTT TCTCTTCTACTGGTCTTTCTTTTGCTTTTGCCAGCCACTATGCTGCT
WI-8853	79	C T	CCCGGCATTG AGGATA	AGTCTTCCCTGA GCCTTCCAT	ACTTTCTTAGCTGAGCAACCTCATCTCTTAGCTTCTGGTTGATAACGCTGTTAATCCCCGGG CAATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52	A G	---	---	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTCGAACA[A/G]ACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCATATAAA
WI-8865a	42	T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T/C]GGTCGAACAAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCATATAAA
WI-8895	32	A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAA[T/A]CTCCCCCTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTTC
WI-8456	93	G C	---	---	CCTTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTACACA[G/C]TTATGTCAAGTTAATATAAACATTTCTAAGTGCTCACTC TCAACTCTGTGTATCTTGCCATGGTCCAGTAACAGTTTACACGGCAGACCACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCGCTCAGTCACCCAC
WI-8496b	157	A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAA[T/G]ATTGTATCAGTGCATATTTCTATGGAAA ATTATATCTCAAGTAAC TAGCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAA[T/G]ATTGTATCAGTGCATATTTCTATGG AAAAATCATATCTCAAGTAAC TAGCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCCCTCTGCGCTTGTCAACCCACATCCACAGAGCA GCCCTAGTGCAGGTGCAGCCACTGCAACCCACGGCACACGGGAACAGGACCCCATGCTGC

WI-12108	40 C T A T A	TGAAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC/TGAAATACTTTTCATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29 G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAAAACGTCCACAAAGGTACAGGCA/GA/CGTACATACGGTCTGTATATACCCCATATATTAC CCCTTCATGTCCTAAAGAAAGACATTTCTCTTAGAGATTTTCAATTTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCCCTCCATCTTTTCTTGGGTGAGGACACC
WI-12201	61 C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCTCTGGAGTGTATGTCCCAAGCCCACTGATCACCTGCATG/C/TGCCA GGTATGGTCGGGGTGTGACGTGGGTTTGACAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31 A T T C T G A C T T	GGCAGGCAGC	GGAGAGTAC AGAAACAGAG AG	TTTTATCTGTCAAGCAGCAGCTCTGACTT/A/TCTCTCTGTTCTGTCTCTCTCTCCCCACATACCA ACTTCTTACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G C C T C	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTCGTTTGTAAATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTC/A/G/GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAGT	TCTTTTCTCTTT TGGTAGTGGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTACGGTTTCTAACCCAGCTGAAAAATTCAAAATA CATGCCCTTTAAGGATTAAGTTTAA/G/CCACACTACCAAAAGAGAAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTTCTGTATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTTGTTCTGCTCATAATTT/C/CCAATAATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAAAT	AGGTTTGAAAA TATGTATTAG TACTTTGT	CTGACAGACTTCAAAAGCAAATTCAC/G/A/CTTCCAGAATACAAAGTACTTAATACATATTTTCAAAAG CTGTTTGCAATTCAAAACAAAGTTAGCGTTTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T	TTAAATCCACACTGAAGATCTGGAGTATGGGGGATATAGGAATTTTCAGCATATGTTATTATC/T/] TGAACATAATTTACAAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCCCTCCCGT GGG	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAAGGGAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA/C/TJAGGGCCACGGGAGGGTGGGGAGAGACGACACTTTTTCCTGGG AAAGG
WI-11321	67 A G T T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAATAAATTTTTTTAA/ A/G/AAGGTTTAGCTATTCCCAATGCTATTTAATACAAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40 C G T G T G C C C A	GGATAAATCA TGTCGCCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA/C/G/JAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTACTGAAGAAGTTATCTGTCTTGTC

WI-11352a	69	T C G	AGCAGCAGC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTTCTGTTTCCAGAAAGGAGAGAGAGTCACTACATAAGCACAGCACACATAGTGGAA AGTCGCTAAGTGTCTACGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCATTGCAATCACCTGTGAACCTATGAAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTAGC/CTGTGCTCAGCGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCTATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAGACTTTCATATCTTGTTTTTAAAAAGTC TCTTCAGTC/CTAGGAAAAAAGCTACAGATTAAAAAATATGACCATGACTAGAAATAGAATCAGC
WI-11388	88	C A	AAGTTC	TGCTTGATC CAAGTTAAAT	TCATGTGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAAGTTC/ATATAATTTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T G	ATAAATAC	GTACATTCACG TGTTTTGTAAA	TTCTATCATTCATTAAAAATGGCAGGTTATGTGTTCTTGAACCTTTAATAAATAC/CTGTTTTTACA AAACACGTGAATGACTTTCTTGTGCAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCOCAGA
WI-11396	52	A T	TTTGTGTTTG AAATGGTGT	AGCTTATTTC ATATTCACCCA	AAAGAAATAGATGGCATTTGTTTCAGTTAAATTTGTTTTTGAATGGTGTTTTATGATGGGTGAATA TGAAATAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTGAITTTTGAACCGTTGTCAT
WI-11441	100	C A	CAGC	TGOCAGGGCCT TATTG	CTGTGAGCTTTTCCCAACTAAACCGTAGTTCCAGTATGTCTGGAGCAGCTGTGCTTGTCTGGTG TATCCCATTACTGAATCCCAACCAACCAGC/C/ACAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T	TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTTATTTTGCAG/CTCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACCTTTCTATTATCTATTATCTCTCACATACATTT CATGTAACCTG
WI-13364	35	A G	TTTTCTTTTGTGCTCTTTTTTTTAGTAGAAGC/CTGGAACAGTTGTCAATACTACCTTCTGTGTTG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAATAATGTCA
WI-11276	41	A G	GGCAGCAGG AGCAGAC	TGTACTGAGGA GOXGGTG	AGGCAACACTGCTTTATTAGGCGGGCAGCCAGGAGCAGAC/CTGACCGGCTCTCAGTACACATTT OCCCCACCCCTGCTCGGTGCTCCCACTCAGGGCTGGGCATGGAGGGGCGAGCGTAGGTCTGGAA
WI-12210	76	A G	CACTATTGC	TGCTAGTTTC ATATGTTTTCC	ATTGGAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACA CTATTGCAT/AGTGGAAAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	AATGGTCTGGTTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGTACAAAAATTACA GGTGGTTTAGTTCAATACATG/AGTACAAATCATTAGAGTCTTTTACAAGTCAATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTTGAT GGAAAGACAC	AACTAAACCA CCTGTAATTTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G G TGGGGCTT	GAGAACACIT GTGGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTGAGTGGTTCTAAAACCTTGAGCTTGCAGAGAACACTTTGGGGCTTTA/ GTTCAACATGAGCTAGTGGTCCACCCAGATTTCTAACTGGTAGGTCTGGGGTG
WI-12345	37 C A AAAGAGGAA	GTGGCAGGAA TTCAGG	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGA[C/A]CCTGAACCCCTCTGCAAGTATCTCT TTCTGACCAGCTGGGCTTGGGACTTTGAGATTGCAAAA
WI-13416	71 C A AAA	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTTCAA	GAAAAGGCTGTAATTTTATTTCAAATTTTGGAAAGTTTTCAGAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTTCAATTGAACATAAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46 G A AAAAGC	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTGGGTCTT AAA	TTTGAAAAGATGCTGAATTTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGGACCCCAACATA TTTAAACATCTCTTACACATACAGAATTTTCAGTTTACAATATTTCCAGAAGGCAATTTTCTTAAGCAG T
WI-12086	72 C T TTGGATTT	CCGGGAAAC TTGGATTT	GGAGTCTGGG GTCITGG	GAACCGAGCTTTATTGGAGCAAAGAGTGTGGACACTGTTTACAACAAACGTTTCCGGGAAAACCTTG GATTT[C/T]CCAAAGACCCGAAGACTCCTCCAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCTTAGCT
WI-11549	102 T G TTTTATG	GGCATAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCCC	ATGCTTTCACAGGTTGATTTTGTAAAGAGTTTGTCTATCTAAATTTTCATATTTATTGGCATAAAGT TCATAATATTTCTTTTATGATCTTTAAATATCTG[T/G]GGGGATTGTACAGACTTTTCCCTC
WI-11585	79 T C AAACAAAA	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACITTC	TTAGAGGAAAGAAATAAACACGGTAATGGGAAATCAGTTCAGAGGTAGGAAGGAGCTGGGTT TGCAAAAACAAA[T/C]GGAAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAAAGAGCGGGGTAGAGT TT
WI-11604	68 G C ---		---	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/CJAGAACTAGGGACTTTTCCATGAAAAATAATTAAGAGCTAAGGAATTCAGCGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108 C A ---		---	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAAGTAAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAAC[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G CAGCTGCTTG	CCAGAAGACT CAGCTGCTTG	AGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAAGAACAGAAAGTAAATCCAGAAGACTCAGCTGCTTGAGJGG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C ---		---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAAA[T/C]TACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTTTGCTAC AAGAACAATAATGGCAATGA

WI-11626a	39	T C C A C T G G A A C A T G A A G G T A G	G T G G T A T G G C T A A T T T C T T A T T A T T A A G T	T T G A T T T T A C T A A G G T C T T C C A C T G G A A C A T G A A G G T A G [G/A] G A T A A G T G T A C A G G A T A A T A T A C T C A G A T A T T T T A A A A T A A A T T A C T T A A T A A T A A G A A A T T A G C C A T A C C A C A T T G T T C C A T T T G C T A C A A G A A C A A A T T G G C A A T G A
WI-11627	23	T C C T T C C T T C C C A T T G C A A C C C A T C T C A A G	C A T T T G C A A C C C A T C T C A A G	A C C C C T T T C C T T C C A T G C C T C T [C/G] C T T G A G A T G G G T T G C A A T G G G A A G G A A G A A A A A A A G G G A G A T G A A A A T A C T A G C C T T T T T G T C T G G C T A C T T C C A T T C G C A T G T C A A G T C C A T C C A T G
WI-11636	61	G G A C T T A A A A A G A T C T G C T T A G T C C T	A G A A C T T G C T A A A T A T T T T A T G T A A C A C T	T C A G A A A T G T T G C A A G C A A A T A C T A T T T G T A A A G G T G G A C T T A A A A A G A T C T G C T T A T C C T T A [G/J] T A T A T C C A C A T A A C T C T A G T G T T A C A T A A A A T A T T A G C A A G T T T C T G T G A C A G G T G C T C A G T A A A C A C T T T G A C T C C T T T T T T G G T A
WI-11537	119	A T T G C T C A T C T T A C T C T G A C C A T	G A C C C A G C A A A A A G A A T G A T T	G T A C C A T T T C T A T G G T G G C A A A T A A G C A A A C T G T G A G T A A A C G A G G G C A G C T G A T A A A T T T A C A G T A T A C A A T A T T A G A G A A T A T T A T G T T G C A A T T G C T C A T C T T A C T C T G A C C A T [C/G] A T A A T C A T T C T T T T T G C T G G G T C C A G G A C C
WI-11654	37	G C C A A A A G A C T A T T C A G C A A C T G	G G C T C T C C C A G G A C A G T T	A G T A G A A C A T C A G T G C C A A A G A C A T T A T C A G C A A C T G [G/C] A A A C T G T C T G G G A G A G C C A C T C C A G A G C T A T T T C T A A G A C T T T C T G T G G T T T C A T A C T C T A C T C A G A G T T C A C A C T A T A T T T C A T A T T T T T A T T T T G G G T T G G G T
WI-11656	28	A A G G A A C T G C A A A A A	C A A G G C T T T G T C C T C A A G T A A A	A C C T G A T T G A T T T T A G A A G G A A C T G C A A [G/A] C T T T A C T T G A G G A C A A A G C C T T G C C T G C A G T T G T T T A A A A T G T C C T G A A A C A A T C A G A T T C C C A G C C T G G A T
WI-11680	55	T C C A A A A G A C T A T T C A G C A A C T G	...	A C A G A T A C T T T T C C A C G C A A C A T T T C T G A A A T G A A G C T T T G A T T C T C C C C T T T [C/G] T T G C A T A A A G G C T G G G A A G G T G G T T G C C A G A C C G T A C A T C T T T T
WI-11696	47	T T A T C A C A G C A G G G A C A G A	G G C A T T A G A G A A G C C A A C C T T	G T C C A A G A A C A A A G A T A C T T T G A C A T C T T T A T C A C A G C A G G G A C A G [T/C] A A G G T T G G C T T C T A A T G C C C A C C A T C T T G T G T T T T C A G A A T C T T T C C A C T T C G C C
WI-11702	69	G A A T A A T A C T G A A A T A A C C A C A G C A G	A G A A C A A C T T A A G C A A A T T A T A C T G A A A	T T A C A T G T G T C A A T G G T G A C A T A C T T T C A A T A A T T A A A A T C G A A T A A T A C T G A A A T A A C C A C A G C A G [C/T] T T T C A G T A A T T T G C T T A A G T T G T T C T A G A A A A C A C A C T G C T A A T T T T T T G T T C T G C A G A
WI-11706	60	T G G C T G G A A T T T T C T C T T C T T T	A T C A C C A A A G A A C A A A T T C C A	T G C T G A T T C A T C G C T T C A C C A T C T G G C T G G A A T T T T C T C T T C T T G T A C A A T T A T T T G C [C/T] G G C T G G A A T T T G T C T T T G G T G A T T T G C C C C T T G C T G C T
WI-11709	105	A A A G C T T G C T T C A G T T T G C A	T C A T T C T T C T A A T T T A C G G G A	A A T A T C A T C A C T C A T A T C A G G C A T G T T T A T A A A A T G A G A G A T T A T G T C C T T T T T G G C A T A C T T C A T C T T C T T C A G G A C A C A G A G A A G C T T G C T T C A G T T G C [T/A] G T C C C G T A A A A T T A G A A G A A A T G A A T G G C C A G A T G G A T G G A A A A
WI-11710	103	G C A C C T A G C C T C A G T C T T C A	G T G T G G A G G A G G G A G G A G	T T A T A C C A T C A A C C T G T C C C C A G C T T T C C A G C A C A A C A G C A G C C A C A C T C T A G A C A C G C C T T C A C T C C A G T C C A T T C T G G C A C C T A G C C T A G C T C A G T C T T C A C [C/A] C T C C T C C C T C C C A C A C A C T C C T T C

WI-11715b	123 C T	AGGCTGGCTGC AGCTT	TCOCATCCTG TGGCT	AGAATGGAGCTGTTGGGAGGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAAAGAGGCTGGCTGCAGCTTC/TJAGCCAC AGGATGGGGACTGGGGAAGA
WI-11715a	49 A C AAA	GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGGACATGCACACAATGTAAACAGACAAA/C/JTGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGGACTGGGGAAGA
WI-11727	43 G C TCAACA	AACAATCCTT AAAACAACATA	CCTGTGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAAATCCTTAAACAACATATCAACA/G/CJCTGCAACACAAAACACAGGC AAATGAAAAACAGATGCCCCAGACAGACACCCACCACATGGCACACAC
WI-11728	16 C G ...	ATCTGTGTTT TCGCTG	...	TTTATTATCAAACT/C/GJCAATCCATTTTCACAAAATGTAAGTTATCATCAGTCCCCATCCACTTT CTCCATCTTCTATCTCTTCCCACTTCTCTCCCTACACTTCTCTCCCTACACCCGGTTCCAAA
WI-11758	61 A G TCGCTG	ATCTGTGTTT TCGCTG	TGATGGCCCT GTGGTCTA	TTTTCCCTCTTTTATTAAGTCGCTACTACTAAGAGGAGAACTGTGGTTTTCGCTG/JGTAG ACCACAGGGCCAAATCACCACAGCTTCTTGTAGAGAACATGGAGAGTCCCAAGATCACCATCA
WI-11295	37 A G AATATAA	GCCTCACAAA GTATTTCTAA	AAAAGTGCTCA TCTGTGAATC T	CCGGCTCACAAAGTATTTCTAAAATATAATTTGCTT/GJTAGAGTTACAGATGAGCACTTTTCA CATTAGTGATATGCAACAAATCACTATTGGCTCAGCAGGAACAGACTTTT
WI-11773	93 T C ...	GGCTCAGAGA GCAAGGGAA	...	AGCATGATATCTGCCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAAGAAAT ATTATTGCCTCTTTTTCCTCCCT/C/GJGTGATTGTTAATAGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G CCAACTTACC	GGCTCAGAGA GCAAGGGAA	AAACTCAGA CTGTAAATTTT GTGTG	CATGACAACTCTTTTATTTAATGGCTCAGAGAGCAAGGGA/C/GJACACAAAAATTTACAGTCTGA GTTTTGCGCGCAGAGACCCCTCTCCACCTTTTCATGCCTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G AAACCTCTG	CCCAACTTACC AAACCTCTG	CGTAGGGGAG GCTAAGC	TAATTCACCCAACTTACCAACCTCTGT/GJGCTTAGCCTCGCCTACCATGTCTCAGAGCAC TTACATTAACTACAATGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A AGTATACA	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATTCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG/C/JAGT GATTTTCTCTCTTTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91 C T AAGTTTAAA	GTTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAATTTCCATTTCTCCCTTTTATAGTTTTTAAATGTGGTATTAGAAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTTCTA/C/JTGTGACAGCAGAGTCTTCAAAGTTTGTATAGACAATCTGA AAATGGGTTCTGAAC
WI-11906	52 A G ATCTGAA	TGTTATAACAT CAAGAAAGA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT/GJTGAGGGAACTG CAGAAATTAAACTTTCAGTCTAATCTCAGATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTAAATGGCTATTTGTGTTG GGTGGTCAAGAGTCTATTTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTGCCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACCTTTGTCTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACTTCTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCCTCTGGGAAGAGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTTCTTGGTTGAAGATCAGATCTCTGGTTTATTTAA[T/ G]ATCAACATTCAACACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACACTGCAGAAAGGGCAGGACAAAAACAAATCACTTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAT[A/JAATAAAAAATCTGTAAACACATTTCTCATTTCTCTTACGA ATACTTCTTTTGTATTTGCAAAATCTATGGCATAACAGAGGCCCTCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAACAAATTTCAACCTCTGTGGTTCAAAATATTTAAGGATCTTGTACCTTT GTGTTTATTTCTGTTTCAACTAAGGA[C/T]AGACTTCAGAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCAITTTAGGAAGGAACATTTCAAAAGCCCCAA
WI-15488	69 C T	AAAAGGACAG CCAGATATCA TAC	TTTCCATCTTA TTTCATTCTG TAAC	CAACATTTATCAACATGGTAGGAAAAAGTTCTCACTCTGCACATAAAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC OGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAGGTAACCTTTTCCCATTTTACAGACAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTA C[C/T]GTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAAGGAA
WI-11070a	110 G T	CAGAAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTGCTT TCAAGTAAAAATTTGACTGAGCAGAAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAAGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTGTTGAGACAGTATTTTGGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT[C/C]CTCTTTTAGC ACGTTCTTTGTTCTCCTG

WI-11076b	142 G A ---			---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTTATCTTCTGGAGGCCTCAGGAACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAGAAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGATTTCTCTCAAGGAACCTCACTCACTGTGCATG
WI-11076a	106 T C AGGCA	AAGGGGAGC	TCCTGCTCTGG	GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTTATCTTCTGGAGGCCTCAGGAACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAGAGAAAGAGAGAGAGAGTCCACACATTTTAAATGATGATTTCTCTCAAGGAACCTCACTCACTGTGCATG
WI-14263	49 T C GGCATATTCA	CGCAGAAAA	AATTAGTATGG	GACA	ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAAT[C/G]GTCCCATACTAATTTTGAATAACCTAACCTCTCCCTTTGTTTCTACTAAGAGAGTTTCTTTTGGCTACAAGTAACA
WI-14267	28 T C ---		---	---	AATTATTGCTGAAATTAGGAAGGAGCA[C/G]TGAATGGGAAGGGGAGGTTAGAGAAGACAGAGATTTAAAGAAAGCAAGTACCATTTTCCAAGTATAAAACTCGTA
WI-13892	50 G A TAGAAC	CTTTTCATTTT	TGATGATGTCA	TATACTAAAA	GATTTGTTTATTTCATCTCGCTTTTCAATTTTGTCTTTTAAATAGAAC[A/G]CTTTTGAATTTTAGTATATGACATCATCATGATGAATTTTCTCTTACTTTGTATTTAGGCTCCACCTCAGTAGTTTGACAAAGGTAGAATGAGTTCA
WI-15288	108 C G TCCCTCTCTC	CATGAGAGGA	AAAAGCTTCTT	TCCCTTGGGA	ACCTCTTTCTGATGACACTTGTACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGGCTACAATTCAGGATGCAGGGCATGAGAGGATTCCTCTCTC[G/G]TCCAAGGAAAGAAAGCTTTTGGCTAATAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATGGCTTCTGTTAATTTCTGGAGCA[G/C]ATTCAAGCAGCAAAATATTTACTGAACACTTGTCTATGTGCTG
WI-13951b	88 G C ---		---	---	G
WI-13951a	39 C T CAAAA	GGAGTGAACA	TTCTCTGATC	TGGGGTCT	AATAAATGGAAGAAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCAAGATCAGAGGAAGAGATGGCTTTCTGTTAATTTCTGGAGCAGATTCAAGCAGCAAAATATTTACTGAACACTTGTCTATGTGCTG
WI-13264	25 G A TTGCCCCAT	AAAAAGGCTC	GGAGGGAGAG	ACGGGAATA	GAGACAAAAAAGGCTCTTGCCCAT[G/A]TATCCCGTCTCTCCCTCCTGACTGACCCCAAGTGTCTTACAATGAACATCCCTCAGCCCCCATGGCATGGTGATCCCCCTTCTCTTGGGATCTGTGAATATAACCAACTGTCTTGTCATGGC
WI-13960	39 A C TGATAGA	AGCAAAAGGA	CATGAAAGGA	C	TTATTTGTCAATTAGCAAAAGGAAGTTAAATACTGATAG[A/C]GATGCAAAATTTGTCCCTTTCATGCA
WI-15843	62 C T CAG	ATCTTATAACC	CTCTGGCTCAG	ACTTGCTCT	TTTGTGGAGCAAGTACTAATTTGTTTCACTGTCTATTTCCCTCACAAGGAGTTGAGCCCCCTAGATGACAACCTTTTATTGTTTAGTCCCAAGTACCTTTATGCATCTTATAACCAAGAGCCTTTCAG[C/T]AGAGCAAGTCTGAGCCAGAGGTTTATACACTTTTGCTCAGGGTCCACCAAGGAAACCAAGGCTTGGCT

WI-13983	52	G A	TCTCTCCACT CCTTAAACCT	CAATACTCTCT TAGCCCAAGTGG	TTGTGTATCTGATTCCGAAACATAGAAAATCTCTCTCCACTCTCTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACACTGACTTACAGAAATTAGAACATCCAGGCACTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTTTAAACACAGCCAT[G/G]TTACAAAACATTGT CAGGGAACATTACAGAATAAATAAGATGGACTTGCAGGTGTAAAAGATTACACTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCTCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGTATG/C]TTTCCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAAGGCCGCCGAAAATATGAGTGAGACTCA
WI-14284	55	C T ---	---	---	ATTTCAAAACAAATCCAGAACAGTTCTCACACTTTGAGCCCTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C C C C A G A T	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAATCTT	ATGACCAGACCAGAAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATACCTGGGTGGAGGGATA CCGCTGCTATCCAGAT[G/C]AAGATTTGGTGAAGGAGACCATGACAGATGACAAAACGG
WI-13522	33	C T A C A A C	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGATGTAGTTACCCCACTAATAACAAC[C/T]GAGAACCACCTGACTTCAAATATTATGAGAG AAATTAATCTCCAGGAAATTTTGCAGAGAGATAATA
WI-13529	42	T C T T A C C A	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCATTCCACAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGTCTCGAGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A ---	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAAACCTAT[G/A]JACAAAACAAAGTATATATTCAGGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C ---	---	---	TGAAAGGATACAGAAAAAATCAGCGAAG[T/C]GAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACAGCTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A ---	---	---	TTTTATTGTTGGTAGAAAAACAGGCTCTTTAACACTGAATAACATCTCAC[G/A]AACTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTGACGCCGGGCCCTTGAATCTGACATTTCAAGTCAC CGTAATAGAAAACAGAGCT
WI-13477b	61	A G ---	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTTGTTTTCAATTAGCTTGTCTTCAAAA[A/G]GAC AGAGAAATAAGATAAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCTCAGTT
WI-13477a	32	A G A G G	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[A/G]CATTGTTTTTATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACITTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[A/T]AAATGTTTCTGAATGTGCACACTAGAATATATGCAGAAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAATATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAAGAAATCAACA TGTGCACAAAAAGAGTAAAAATTT/GJACCAAAAAATTAAGATTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAAATCTAACTGCGCAGAG AAATCAAGACCGATGTGTGAAATCTGGGGAGCTTCAAAATTTCTGCCCTCTAAACATTTTCAC
WI-13857	28 A G	CCAAITTTTCATTATTGCC TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAATTAACCAAAATGT CTGCCCATTTTGTGTAGCTTTTCATACAGTACAGATTTTCATTTGATGTGCTGCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[T/G]TTTACAAACATTGAATAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T	TAAATCAGTCTGTGTCAAGAAAGAACAGGACTTGATCAAGCTCCAGCCCTCACCACCTCTATCAGCA TAGCAATTTTAAAGATCAGAGCTTTGTTTACATTTGTCTAAACCAGAGAGAA[A/T]GGAAATCA ACTCCACAGATCAACATGT
WI-15801a	24 G A	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAATAC[T/G]GCATCCCATCCACTCTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59 T C	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCITTTATCCAAAGATGGGAAGC[G/A]CATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-13578	48 T A AACC	GGCTGGACACT GCAGTGAT	CCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCACACTGGGCTGGACTGCAGTGAATTCAGGG GCAGGTGTGGGCGAGGTGGGCTCTGAGCCGAGGACAATGTCCATGGCAGAGCTTCCAGAA TTTTTTTTTGGTGAGTGTGTCTCAATAAAGAGCAGAAAGAAACC[T/A]AGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTTGATATTTTCCCGAGGGCAAAAAAGA GAGTCTTCCCAGAAACCTC
WI-13789	62 G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTC	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATTTGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGACAGTGGATGTTAGGGTCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACA AAA	CCITTTGGCCA GTACTTTTT	AATAACAAGTTTAAAGTTCCAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCACA AAAAGC[G/A]TGCACAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T ---	---	GTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAAC[CT]GTCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	TCCCCACCCCA CCCT	GTCTCACTTCTTGCTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCCAGAA[CTG]AGGGTGGGTGGGAATACCTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATCCCT
WI-13600	26 G T AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACTTTAATGAGCCAAAGCATCCAT[GT]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAAAGAATACGGATTGTGTAGGGAAGAGCATAGAGGACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89 G T GACAACACA	GCATACCTCAT GACAATATTA ATATTAAT	GATAGGAAAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACA[GT]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCCCCA
WI-13650	76 A T TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTTT	GCATTAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTCAATATTTTAC TTTTAAAC[AT]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[CT]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTTGCATTTTCTAAAA AAAGAAGACATTT[AG]TTTTCAGAGAAAACTGTGGTATCATGCAGGAAAAAGCAGAAAAAAAT
WI-13909c	93 A T ---	---	ACTTAAACTGGCTTATCTTACCGGTAATCTATCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACTC[GT]AATATCTTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA CTCTTCAAACTCGAATATCTTTTTC[AT]GAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTACCGGTAATCTATCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACTC[GT]AATATCTTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ---	---	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC[CT]ATGGGAACCTTGAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78 T C ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCAT[CT]CTGGACCATGGGAACCTTGAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15389b	104 G A AAA	GATGAGGTGAT TCCACACTT	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGAAAGTACCATTTTCAAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[GT]AAGTGTGGGAATCACCTCATCTGTGCG

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGGCTTTTGTGTC[G/A]TTTGAAGACTACCATTTATTCAAAATTTATT ATGTAATACACTCATCCAGATAATGAACACATCTGCGAAAGAAAGTGTGGGAATCACCTCATCTGTGTC TGTAATCTGCTTACAGTCTCTTGGCAAAGACAGACATATGTTTTCATATAAAGATATAAATGCTTCAT TTTAAACTAATTTAGTGTTC[G/T]TTTAAATATATGAACCTTTGGTGAATATGAACCTGTACCAAAAC C
WI-15747	88 T C AGTGTT	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAAGTTTCATA TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTCTCTGTTAAGTGTGGATATACCTGGCTTGACAC[G/T]GGACACCTTTTACG GAGGATTCCGGACAAC
WI-13752b	117 CT ---	---	---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTCTCTGTTAAGTGTGGATATAC[G/T]GGCTTGACCCGGACACCTTTTACG GAGGATTCCGGACAAC
WI-13752a	106 T C AGTGCTGA	CTTCTCGTTA AGTGCTGA	CCCTCCGTA AGGTGTC	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGCTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCAATCAAAACAGTACATGATTAC[G/GCGTTTCCAGAAATCTGGATAC
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAATGGAACCTTCATGCAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGTGTATGGTGTGAACAAAACGTA[G/T]GCTGTGCTTATCTTTTC CTGATTCT
WI-13744	115 CT	TGGTGCTGAAC AAAACCTGAA	GATAAGCACA GC	CCTTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAGAGAGCCCCGTTACATACCTTAT [C/T]AACCATTTCATCCACCATTGTGTAATAATCTCATCTCTGGGTCTGGATACTCAAAAACAGAT
WI-14061	68 CT ---	---	---	TTACAGTTGGATTAACTACACACACTGAATATACTGAATTAACCTTCAACCCCTTTCATCCATTCAG C[A/C]AATTTAAACTCTTGCCCAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-15719	69 A C CATTACG	ACCTTTTCATC CATTACG	TGATACTGGC AAGAGTTTAA ATT	TAATCCATCAATCTAAATCACACATACATAGATCAACAGAAAGTACCACAGTATGCTTTATTTGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACCTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	GGATTTTATTCACATTAACTTGCACAG[G/T]TAGCAAAAAAATCAAAAACATAAAAACATAAGCCACA TATCAAGAACAATATACAATAGAGATTGAATTTCTCAATAGCATTTGGAAGGATTTCATATAAATA TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACACAAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACACAGTG
WI-15736a	27 G T CACA	ATTTATTAC ATTAACCTG	GTTCTTTGATA TGTCGCTTAGT TTT	TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACACAAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACACAGTG
WI-13785d	72 G A ---	---	---	TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC[G/A/C]CAAAATG AACAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56 A C ---	---	---	

WI-13785b	40 C G	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785a	27 T C TGC TT	GGATTTTACAT TCAGCCTAGAT	TGTTGTGACAG CTATGTGTAC T	TCAAAACTGCACACTATAAAAGTGCTTT[C/AAAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG
WI-13793	88 C G ATAGG	GGCAGGAGGA TTTGT TACT	GGCAGGAGGA TTTGT TACT	AGAAACCAAGTATATCATAGGCCAAATAAAATAGTTTTACCCCCATTGATACAACATAAGGGATT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTTCTC	TTCTCACCCT TTTCTTTCTC	AGAATGGGCTC TTAACCTTGT A	TAGTCTCTCTACAATTCCTTCAATCCATTTTCTCTCTCACCCTTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCATTTCTCAACACAAACAAAAACAACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACITTTGAACCATGTGTAGACTGC[C/G]GGCACITTTAGAAAGAAGCTGAGACTGAA AAGTCTGTCTGACTTCCAAAGGAAGGTAAAGTCCCTGTTTGCAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66 G A C	TGAGGTTTTTC ACCCTATTCTT	TTTTTCTCCCC AGGGTCTA	GTCCCTTTCACAAAGTCTCCCAACTGGTTTGAGATTTCCCTTCTGAGGTTTTTACCCCTATTCTTC[C/G/A JTAGACCCCTGGGGAGAAAAACACATGTGTAAAGTGGCTCAGGACATGAGGACGCCGCTTCACAAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C AAT	TCATTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATTT[C/G]AGATCCCAGATTCAGCTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAAATCCTGAACATTTCTTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACTCATCA[C/G]CCTTCTGATTTTGATTTCCCTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATTTCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
WI-13725	56 A C TGGGTGCC	TGAGCACATA TGGGTGCC	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACTTACACATGGTGAGCACATATGGGTGCC[C/G]GCCCGAG ACAGCAGGATAAGTTTCAACAAACTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTCAGGATG
WI-15702d	107 T C	CAAATGTTTTATGAAGAGACTCCGAAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAA[C/T]CTGTAACAACTACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C	CAAATGTTTTATGAAGAGACTCCGAAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAA[C/T]CTGTAACAACTACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T	CAAATGTTTTATGAAGAGACTCCGAAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/T]CTGTAACAACTACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 GC	AACAAAATAA AGGCTTTCAA AAAG	CCTCACCCTT TACCC	CAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTCAAAAAG[G/C]GGGGTAAAGGGGTG AGGAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAATGGTCTTTTGAACAATAAGTTT TGA
WI-13831b	113 TC	---	---	TTTTTTTTATGGATGCACTGTTACATGTTATTTAGCGAAGGTGACTTGGAAAAGGAGATTCACAT ACTCCACTGTATCCTCCGGGTAAGTTTCTCTCTCTGTAGAT[C/G]GTCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13831a	56 GC	---	---	TTTTTTTTATGGATGCACTGTTACATGTTATTTAGCGAAGGTGACTTGGAAAAGGAGATTCACAT CATCTCCACTGTATCCTCCGGGTAAGTTTCTCTCTCTGTAGATGCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13806	62 GA	---	---	TGATTGAGCTTAGAAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACCTAGCCTCAGGT[G/A]C CCATTAAGCATGCTGTGAATGCAAGGAAAAGCTTAAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
WI-14372	86 AG	---	---	CACATTTTCAGCAACAAATCGAGGTGCAACACAGGGTTTATTTACATTATATTAACCTGGATTT TTTGCAAAATAATAGGGA[G/T]CTCTTTAAATAACCATCTCCTCATTTCATGGCCAGT
WI-14373	95 AG	---	---	AGCGTGTTTTTGAGGCTGAGGACCCCAACATGACACGTAAGACTGTAACCATGGTCATGTGAGTT ATGAGCTAGGAACCCCTGGACGAAACCA[G/C]ACATATACAATCATCTCCCACCTCCCAACGCCTTT ACTTTCACAGCCTCTGCA
WI-14078	61 CT	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAGAAACACACATGGTGATCAAGAAAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAAGGACTTTAGATGGTCACG
WI-14083	47 CT	AGACTTGAGA GCTTAAAACA ACACT	GOCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAAAACAACACT[C/T]ATTTGTTATTTTCACAG CTCAGTAGTTTAGAGGTCCAGTAGGCTGGCTGAGTTGTTTGCTTAAGGCTTACAAGGCCAA
WI-14085	31 AG	CATTTATTTTC ATGTGTAAGA AGAAAA	CAGTCAITGTC ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAGAAAGAAAAAC[A/G]TAAGTACGACGTGAACATGACTGCATGGATAC ACGGCTCAGACGAGGCTAAAGTCAGAAAGTGAGTGAAAAACAATAAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCCTT
WI-12169	121 GC	AATAAAACTT CCTATTTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAGGTTGGCAATTTTATTTCCACTTATCAAGAACCTACAAAATATTTTGTTCATTCTAAA TTTTCACCTTTATTGCTAAGTTATAAAATAAACTCCTATTTCTTTTGCTT[G/C]TTTTTTCTTTCA CCTCAGAACCCCTTA
WI-15705	50 AG	GGAGGGAGAT TTTAGACTGA ATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTTGGGGAGAAATGAAGGAGGAGGAGATTTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCCTCTCTCTTTGTACTACGGAGACCCTGCTTATAGCCCCCAACAGGAAATCCTCA TCTGGGTTGCCAGACAG

WI-14379	102 C T	TCTATTAAACA GGGTTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA	TTTATGCTGTTGTTTCTACTGGTGGTCTGCTCACTAATATCAATCCTAGTAGTATTTCTTT TACTTGTGCTATTACAGGGTTATGTCACACC[C/T]GTCAACCTCAAACAGATGATACT TAAATAAAACAAGCAGAAAA[C/A]CCCACTTAACAAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGGGAGGCTGGCGAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	CGCAGAGCTG CTGTATTTAAA A	---	ACCGCAGAGCTGCTGTATTTAAA[A/G]ACAAGCTGTGGAITCTCTCAGGGGCTGGGACCAGCTGC AGTGGGGGCTCCGGCACTGCTCTCTCTCCAGGACTCTTCCGACCAACCC
WI-15937	24 A G A	AAACTGAAAC GTATTTCTCTC	GCAGAGATCCA GACGCTTGT	TGAACTGAAACGTATTTCTCTCA[A/C]ACACCGTAGAACTTAAGGGCGGCAAGACTCACACCC ACCACCTAGCGGGGCAAAAAAGGAAGTTTCAGGTGATACAAGATGCTCCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A		GGCCTTTAAGT TTCTACGGTG	ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAAACACTAAGCC[A/G]TATTATTCAAATGTGTTTCAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92 A G		---	GACAAAAGCTCAGTCACTAC
WI-14125	88 C T	GGTTGACCTG CATAGATTTT	GGATGGCATG GCCAC	GACAAAAGGGCAGTTTCTGTAGTTCAGCAGGGCCAGAGCAGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTGGACGACTA[C/T]GTGGCCATGCCATTCTGTAGTGAAATTAATGAACA
WI-14136	120 G A	GCCTTCTCACC ATGCTTTCACA	CTTGTCTGTC TCTTGGGC	GTTATTTCTCACAGTTCTGAGGTAGAACTGTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGCTTCACAT[G/A]GCCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14138	23 C T	TGTTGGACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	TTGTTGTTGGCACCAGAAAAAGCT[C/T]ATGTTCTATGTTATGTCACCTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-13551	74 G A	TCCTTCAGTAG TAGTATATTCA GACAATC	GCTCATTCTT TTAGTGCTAAG TAATATT	GGCAGGTTTATTCATAATTTCAAACCTTGGAAAGCAACCAAGATGTCTTCAGTAGTAGTATTTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAAGG AACCTTAAATGGATATTACT
WI-15953b	59 C T		---	TTTTTAAAGAGTGCTCTTCACATCATTTATATTGTTATTCACACAAAACTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCC
WI-15953a	26 T G A T	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTG A	TTTTTAAAGAGTGCTCTTCACATCATTTGTTATTTGACACAAAACTTTTTAACTCCGTCAC AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCC

WI-14631	82	G A ---			---	TGAATTCATGGACAGTTTGCCTCTGTTTAGTGAAACCCCTCACAGCACTCTGCATAGTCGGCTTTCTGTCTCTTTAAACG/AJTGCCCTGGTCCCTCTGCCAAACTTTTAGGATTGGCCTCCTCAGGGCCTTGTCCTGA
WI-6053	24	A G ---			---	ATCACCAACCGTGTCTAAGAACAAAC/AJGJCTTCATGTCCAACTCATATCCCCGGGACITTTGTCAACTGCAGTACACTTCTCGCATTGAACCTGGCTTCTGGAGGAAGCCTCTAGAGCCAGGTAAGGGGGTGAGCAGTGAGGGGTATATCTGGGCTGCCAGTGGAAACACGGAG
WI-15964	99	T A CTGGAGGTA	GCTCTCTGTCC	GACTTCTCCAC	CTCTTTGC	CAGAAACCTCTTCTGTGTATTAAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTTGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTA/T/AJGCAAGAGGTGGAGAGTCTTTGGCAAG
WI-12075	103	G A GGCAC	AGCAGCTGGG	CCCCCTCTTC	CTTCTCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAAGCAACAAGCCAGGCAAAATACCCATCAGAGCAGTGACAAGAGCAGCTGGGGGCACGGGGAGGC/G/AJGAAGGAAGAGAAAGAGGGGAGGAGCCT
WI-12179	96	G A TGGAGGTCA	GGAGGTACGG	TCGAATGACCC	TGTAGATGC	TAATTTAAAAACACGCOCTTCCACATAGTGCCTGAGGCATCTGCACATTTTCTAGAGGACATGATAGTGATGTGGAGGTACGGTGGAGGTCA/G/AJGCACTACAGGGTCACTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	CAAGAAATCAT	GGAGATATTGA	CTTTTCTGA	CACAAATAGTGAATATCTGAGCAAGAAATCATCTCTATTTAAAAATTGT/C/GJAAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105	T A ---			---	AATGTGGACTTCAAAACAAGGTTTAAACATACTAATAACAACCTCTACAACACATTTCCAGAGCATATAACAAGAAATATTACAGGCAGCTAATGTATTAAAT/AJAAACCATGAAAGAAAAAAGCTTG
WI-13473	31	C T ---			---	ATCTAGATGTCAGCAAAATGGGCTGAGACTGT/CJTTGTCTGTAGATGCAGTGTGTGTATGTTTCTACTCTATTACAAAAATTAAACAGAAATATGGCTTGTGCAATGTTTATATACAGTC
WI-13967	103	A C AAAATAAAA	AAAAGACTAC	TTGTGTTTCA	TG	AATTTAATAGCAGCTCTGTGTGTGATTTTAAAGAAACAAGATAAAATATGTCATTCAGCAGTCATTTAAAAATAAAAGACTACAGATACAAGGAAATAAAAAA/A/CJACACTTTTAGGAGATGAAAAACACAAA
WI-14408	60	T A G	GCAGACACAC	TTAATTGTGA	TTACTTT	TTAATATTTCAGCAAAAGTTATTGCAACAGGTTGAAAAATGCAGACACACTATTACAGGCTGT/AJAAAGTAAACAATGAGTTTACACAATTAATAATATTAAACATACCTTATGGGATTTGTTGAATGA
WI-13683	47	C G ---			---	TTTTGTGTTAAGAACACAGCATTTTGAAAAATAAAACCTATCTGCCCATG/C/GJTTTACAGCCTTTTAAATTTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C T CGTCT	CACCATGGCA	CATTGAGATAA	CAC	TTAGAAAACTGATAAAAGCAACACAACTTTTGGGAAAGCAACCATGGCAGCTCCTTTGTGCTA/C/TGTGATAAGGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---			---	ACATGGCAGATACAGAGCTGT/C/GJCTTTGAAGACCACTGACCAAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCGTCTGGGAGCGTTGAAGGGTGACCAAGCACATTTGCACATGCAAAA

WI-16002	59 T	GATAACATAA AATGATCATG C AGAATTTG	GCCATCTCCTC TTTGACTTTT	CCAAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGTCATGCTGGCT
WI-15361b	101 A	CCACTTGAAC TCAAGTCATC A G A	AAACTAAAC CTTTGTGCTA AAA	GTGGAATTTTATTAGCCATCAAAATTTCCCTTACACTCAATACTGTTGAACAACAAGATAACACAT CTTCCTGCTCATCCACTTGAACCTCAAGTCATCA[G/T]TTAGGCACAAAGGTTTAGTTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73 T	GC GTTTGACTT G GTGGG	TCCACACTGC OCCG	TGAGTTACAAACAAATGAGCAACAAGTTAGAAAAATTTGGTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGCGAGTGTGGACGGGAGGATTGCAACCCAGAGTTTCATCTG
WI-12535	50 A	CTAGGAGGGTT GAGGTGTAGA T TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTAGGTTGACTAGGAGGGTTGAGGTGTAGATAT[T/C]TTCCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G	AAAGGCACAC A GGGAA	CTCAGCCTGOC TTGACC	TTCCATTATTATGCTTGGCTTACCAATTTTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGTTCAGAAAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T	C ---	---	ACACAATATAATTCATTT[C]CGAGTGATTAAACCTTATTTGTTTAGAACCAACAAACAACTAC AAGAAAAACATTTTCAAACCTTTTTTTTCAGGCTGA
WI-14808	52 T	ACCCACACA CTACCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACAGATTAAAAAGTACCCACCACACTACCCTGTT[A]AAAACTTTAAG ATTGTGATGCCCTCTGCATCAATTTTAGAAAAACAAGAAAAACACAACCTGAAGGCCCCCATGTA AGTTAAAAAAAATCGAGTCAGCAATTTATT[T]AAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCAATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-14816	29 A	T ---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542c	71 G	T ---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G	T ---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C	TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C	GGATACAGCA GTAAAGAATA CAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTTCTAGAAACTGGGGATACAGCAGTAAAGAAATACAAAAAATCCTGC[C/T]CTTATA GAGCATACATTTCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28	T C	---	---	TCTTTGGAGGGATAGAGGACAGAGTGTTC/GTTGATTTTTCGTTTCGGTTTCAGTTTGGTTGTCATT GGTTTTTGTITTTTGCTAATTTTGGCCCAACCCTATAAAAAGCAGTGCACCCAGAGGCAG
WI-14856	60	A T A A	---	---	ACATTTCCCTTATGATAGCAACAACAACTAAATATGATGATGTGTGACACGGAAAAATACCTTAATATTTAA AGTTTGTAAAAAGTAGCAAAACAAAAATTTGAGTATATACTATAAGTATAGAGGATGATATGAAAAA GGCTATAAAAAAGCTCCAAAA
WI-14863	61	G A	---	---	ATGGCAATTTACTTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTCTG/G/AJAG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGGCCACT ACCTGGC
WI-14867	46	T C A	---	---	TTTTAATTAAACGTAAAAAGGCAGGACATCCAAAGGCTCTCTAACA/T/CJGAGTGTCTGCAGCCCCA TTCGCTTTGAGATGTGAATGTGTTAACCCAGGGTGA
WI-14733	98	G A A	---	---	ACGGAGTGTCTCTGATGATATCTTTGTCAAAAAATGTTTGCCTGATTCTTAATCATGAAAGAACAATT AGAAAAAATCCAAATGACAGATATTCTGCA/G/AJAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79	A C	---	---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAGGTGCCACTAAGGAAA ACTTCTCCATTA/CJAAGCTGCCTGTGTGCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GCCTGTGTTCTGTCTT
WI-14898a	50	A C A	---	---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATACJAGGTGCCACTAAGG AAACCTTCTCCATAAAGCTGCCTGTGTGCACGTTGCCCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTTCTGTCTT
WI-14907	48	G A	---	---	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTTGGACTCTGAC/G/AJATTCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCATCAATCAGTGACTCCTGCAGTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52	G A C	---	---	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCACTTCTGTC/G/AJAAGGTCTTTTC CTGGTTTGCAGACAGATACCTTGTCTGTATCTCCTCACATGGCAGAGAAAGAGAGAAATAATCT
WI-14913	88	C A	---	---	CTGATGCTTTGACATCTGGGCAATTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGCCAAATTC TAGTGATAGTAGAGGACTCA/CJAJCCTGCACGTGCACCTTTCTATATACAGATCAACCAATCCAAAAAC CTACACCTCCAACCACT
WI-14914	66	G C A	---	---	ATTTCCCTTGATTGGCTGTCTGTAAGCCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA/G/ C/GAATTTATGTCTGGCTTGTGATGGCTTTTACAGC
WI-14926	49	T C	---	---	GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACCTAGCGAAT/CJACTTGTGGACCACA AGACTTGTGTGAGAACATGTTCAAAGACAGTTTTTCAATAAAAAATTTTCCTTAATCAGGTCCA

WI-16083	89	C	T	AAGGAT	CAAACATATC	ATGTTTAAACA	TGGAAGAGATT CCAGCCC	GCATCTTTATTACCACAGAAACTCATTTATGTCTTAAATCATTGTTTAAATATATAATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAAACCATC CATTAAGCAG
WI-14930	55	C	T	CTCATGGAT	GGAGGAGTCC	GGAGGAGTCC	CACAACCAACC AATACCGC	CAGTCTGTGTCTGGAACAGCTCTCTTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGTGTGATTGGGGAGCACAGGGAGGCA
WI-14946	47	T	C	---	---	---	---	TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCAGACATAACA[T/C]CTCTAAATCATCTCTA GATCAGGGAGTCATAAGGACCATTAAAGGCTCATTACACACAGTACTTTATGGAAGGATT
WI-15987b	80	A	G	---	---	---	---	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTTGGTAGTGCCCTTCCACTATGTGAGGACAC TAAGAAAGATGGT[C/A]GTCTATGAACCAAGCTGCCGGTCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C	T	GGGTCCCA	CACAATTAAA	GGAGGCACTA	CCAACCTC	ACATTAAACAGCACAAATTAAGGGTCCCA[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAAGATGGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T	C	G	CTAACTTGTCA	ATCAGTTGTG	GA	GAATAAGTTCTTATGCCGTTCCCTCAGGGAACAGGGAACCTGCTAACTTGTCA[T/C]TCCAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGCTTCCCTCCAGCTGA
WI-16100	52	A	G	TGA	CAAAAAGCTA	ACAGGAATGTC	AGAAAACAGT ATATTAC	TTGTGTTAAATCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATTCCTGTTATCAACTCTCTGAAAATC
WI-14958	83	A	G	CAAGG	AATAATTTAT	AATGCATTAT	TTGGGTTTT	GTGATTGATCTGTAATTTATGGGATTATTTATCAACTCTAAATCCAAAGATGAAAATAATTTATCT CTTCTTTCAAGGG[A/G]AAAAACCCAAATGAATGCAATTTTCAAGTTTCTCCAGGCCTTTGAACTGC AGCAGAAAATTCAGGA
WI-14976	35	C	T	TCGTTCAAAG	GTTGATTGCT	CTTCCATTCTA	AGC	TATTTTTTAATTGGTTGATTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGCCACACAAGAAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31	G	T	T	TCAGTGGTGT	CACCTCTGACA	ATAAA	TAATTGATTCAAGTGGTGTATTGGATT[T/G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTCACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C	T	GAAGCTGCAG	TGCATTAAAT	GCTATGTGCTC	AGCTTTCCCT	TGATTACATTTTTTAAATCATGCTTACCAGCCCATCTAAGCCAAATTCAAACACCCTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAGAAACGTA
WI-15002	72	T	A	---	---	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATACAAATGCACCTGAAAATGCCTTCTTGA TTTCC[T/A]TTTCAGTTTAGGCTCAATGGGCTCTCCTCAAGGCTGACCTCAAAAGGCCAGTT
WI-15000	90	G	A	GTCTAA	GACAGAAAAA	GTTTCTAGTTC	CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACTT CATGTACCTAT GAAATAA	CAC TGGACATA TTCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTTTTATACACAATACTTCTATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCAGTGCAGAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAGAATCTAC
WI-13470	100	C A T	CTGCGCTTTAT ATTGGAATTC A T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCTTTATATTGGAATTTCTA[C/A]JAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCCCTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA[T/A]JTCACAATACCATATACAAACATACT TTCAATCACAACTCAAAATATAAAATAACCTACAAAATCACATTGC
WI-13712	40	A C TCTATTG	TTTACTTTGTT GTCAATTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTACTTTGTTGTCTTTTATTCTATTG[A/C]JATTATAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTGTTAAATTTATGCAT
WI-16163	35	C T A	TCGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACCTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA[C/T]JATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTTAAAGAGGACTATTCTTTAAACAAAGACAGTGTCTGCACATTTATTTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGTCTCT TC	TCAGATTTTTA CATCTCTTTCT AGCA	TTTTTTTATTTGCATTTGAGTGCTTTATTATATTGGGAATTTGCAGTGATATTAACTTTGTACAAAT GCACAAATCTTGCTCTCTT[C/T]JTGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58	T C GATTTT	CGCACTCTAA ATTAGAGATA C	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTTTCTGATATACATTT[C/C]CATCTT ATTCACCAACGAGCACACCCACGACAGTAGAACAGTTCCACACCTGATAAAATGCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTTCCCAAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATTTCCAGTATCATGTAC GCACTAAAAAA[T/C]GTGTGCTTGTGCTGTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C CCCAGAGTCGC	TGAAGATTAA CCCAGAGTCGC GCAGCAAGAT TACATCAGTA	AATTGTGTGCA TTTTGAAGAGA CTCCAAATAGC CTAGAGTATAG	ATCTGGTATTTGTGTATCCCAACAGTATACAGAACTACTCTATAAAACCAACCCACCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC[A/C]TCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T ATGT	GCAGCAAGAT TACATCAGTA ATGT	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATAATAACAGCTTTTTTTCATTGAAGCTTTTGTACCT TACTATACTCTAGGCTATTTGGAGTGTTCCTCCAC

WI-15100	74	G A ---				TCCTATTACAGCCAAAGAAAATACCCAAATTATTTCCAAATAAGCAAAAATTTGGAACAGACTGGA GTGAGAAAC[G/A]GGTTCCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T AATTACT	CCCTTATTTTC CCAAATATAA	GTCACCATGTT ATATTTCTTT TAAGAC		TGGTACAGAATGTTTAAATTACAGCAGGGCAGTGATTCAGTTAAATAAAATTAACATGGTGACAGCTTT CCCAATATAAAATTACTAAATTAA[A/T]GTCTTAAAGAAAATATAACATGGTGACAGCTTT TCCTTAATTTTATCGGAATCCAGGACACAACAAAGAAAACCCCAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[C]GCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGTGAGAC AG
WI-12002c	89	T C ---			---	TCCTTAATTTTATCGGAATCCAGGACACAACAAAGAAAACACCCCAAAACCCACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGTGAGAC AG
WI-12002b	68	G A ---	TCGGAATCCA GGACACAA	TGGTTTTGGG TGTTTTCTT	---	TCCTTAATTTTATCGGAATCCAGGACACAAC[C/G]AAGAAAACACCCCAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGTGAGAC AG
WI-12002a	30	C G	GGGAGCCCTA GTTGCAGTAA	CCTGAATATGC AATTATTTATT ATGACA		TTTTCAATTTATTTCCAGAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTATATAATAATAATTCATATTCAGGATTTTG TGAAATAGGIGATTGGGA
WI-15116	96	C T	GGCCTAAAGG AATGGGA	TCAAGCGACCA CCAACAC		GCAAAAGCAAAGCTATGGAGGCCTAAAGGAATGGGA[C/T]GTGTTGGTGCTTGATACCTTGGT GCTTGTGTGCATGGAGCAGAAAGTCTTCTGGTCCATGCAGGGGCTCACATATTTAACTGCACATAAT TTGGCAAACTGTCTATTC
WI-15153	40	A G	CCCTTATGTTG GCATTGCA	AACCTCAGATA AGTGCAGTGC T		ATTTACAGTTGGCCAAAGATCTCCCTTATGTTGGCATTGCA[G/A]GAGACACTGCACCTTATCTGAGGTTA GAAAAAATGATAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTAACATTTCTAA
WI-15215	84	G C	TGGCTTTAGAA TCAAATGGG	CCAACAGGGGA AAAAGTCA		CCTTTGCTCTCTGAACCTGGGACCAAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTAGAATCAAATGGG[G/C]TGACTTTTTCCCTGTTGGTGGAAAACCTGTGAGGGTTTGGCA
WI-15225	80	C T C	CTTGAGGACCT AGAAAGCAAA	TTTGATTGGCA TAATCACTCC		AGGAAAGAGTGGTAAAGCAAGCGCATCATTTGGATGGAATGATTATGTGTACAGCAGCCTTGAGGAC CTAGAAAGCAAAAC[C/T]GGAGTGATTATGCCAATCAAAATGCAAGTTGGAGATATGCTAAAA
WI-15152	51	G A ---			---	AATTTGCTAGTGCAAATGGACCCAGAAATGGAAGGGCTATGTAACACACAC[G/A]TATGCACACCAC AGCCATGTCAGTGCACAGATCCTCTTGTGCATTCAGCTTTCTTAAAAACACATCAAAAGGCTGCA
WI-15123	55	C T TAGGATG	TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAAACAGAC		TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAAACAGACATGCAACACGAGATAAAACACAAT

WI-15182	49	C A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACACAGGGCAAAATA[C/A]TGTGGATTAAACCC ATGCTAATGGGTTACCTTTATTAGTAATCATGGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGOCCTTGGC ACTATG	ACTTATCOGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGACTATG[C]TACTCTGCTGACGGATAAGTTGGC ATATGGTTACAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCT
WI-12601	42	T C	CATTATTGAG TATCTTGCTT	GTTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCCATTATTAGTATTCTTGCTTTTGA[T/C]GTCTACGTAAAGCATGTAAGACT ACAACATTACGACCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAACAAACATTTTGTCAATTCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCATAACAA	TTGAAAAATGGT TAAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTTAGTGTAGTACACCCACAGATATTTTGGGGAGAAGAG TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAAAT[AT]TGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57	T C	CATTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTTGAATAAACACCATCAT[T/C]CCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCTCTCTCGCTGGTTGACGTTCCAGCGGAGT GAAGCCTTTTCTGGAATG
WI-12634	52	T C	GCATCATATG AACTGTCTAGC	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAAGTGGAGACAGCGCATCATATGAAGTGTCTAGCAGTATTAT[C]GCTATTAGCTA TGTTTACAATTGTCTGAAGGGTCTAGATGTGTACACCCACAGAAAGTGGTATTCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC AA	TTTGTCTGAAGGGCTTGACACAAAGTTCTAACTTT[C]TTGTTAAAAATCTCTGGCTTTCCCTGGCTGG TGAGGAGGCACAGGCTGGGCTTTCAGGTATCCACTGGTGGCCCGCATCTGTCCCTCCACTCCCCAG CCACATCTTGGCTCT
WI-12159	28	C T	AAGACACCGT GCAAAATGC	CCCTCTCCTCA GTGCACCTT	CTGTCCGGGGAAGACACCGTGCAAATGC[C/TA]AAGTGCAGTGGAGAGAGGGAGGGTGTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGAGTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAAATGCCCTAGTGGCATTAAGGATGC[A/G]TAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTACTCCATGTTAGGTGCTTTACTTGGATTATCTCAGTTAAAAACCCACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAAACAACAA AGCCTAAATGG	ATGAGAGGTAAAGTGTCAACAGTAGGCTTAAAAATATTCAGTAAACCATGTGTAAACAGCTGTGC[G/ T]CCATTTAGGCTTTGTTGTTCCATTAGAGAGACAGGAGAGGAAATTTAGCATAATCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGTGCACACAGCGGACACTGTCTATAAGTGAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAAAATCAAGAATGAGCTGGAGAAATTA TCTGT
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCCTCCACCAT GATTGTGA	AAGGTTAATGGACTCACAGTTCCATGTGGCTGGGAGGCT[C/TA]CACAATCATGGTGGAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAAATGAGAGC
WI-13936	123	C T	AGTTGGCATTC AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTAGTATTTTATCCATGGCGCTTCTCACTCCCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCAAGACCTATGACCTGTATCTTCAGTTGGCATTCATAGCCTATC[C/TA]AACTCCATGT GGGAGTTTCATAATAA

WI-14528	62 T	T T T T A A C T T T T T C T G G A T G G T A G T A A A T	C T C G A T T A G C A C T T A T T A T A A A A A T T A A A A	T A T G C T T T A T T G A A G A A A T A G G C T A T T A A T A T A T T T T C T G G A T G G T A T A A A T T G J T T G A A T T A T A A A T T T A A T T T T A T A A T A A G T G C T A A T C G A G A C A T C A C T G G G T A T A A T T G A
WI-15347	74 C	G A C T T C A A A G G A A A G A C A T A A T T T	T C A C T C C C C C A A G T C T T T G	T A T T C T T T C G G T T C G G A T G C A A A C A A A A A T T T T A A A G A A A T G T G A C T T C A A A G G A A A G A A C A A A T T T C J T C A A A G A C T T G G G G A G T G A A G G C A G A G C C T G G T G C A G A T G G A C G A G G T C T G C A G A C G
WI-14546	95 C	C C A A T T T C T A G T G A T A G T A G A G G A C T C A	A A G T G C A C G T G C A G G	G T A T T T C T G A T G C T T G A C A T C T G G G C A T T G C T G T C T A G A G A G A C T A C T T C T C T G G A C C A G C C A A T T T C T A G T A G T A G A G G A C T C A C A J C C T G C A C G T G C A C C T T T C A T A T A C A G A T C A
WI-15353	37 G	A ---	---	T T T A T T G G C T G T C T G T A T A C A A T G T G T G T G A A A A C J G A J T C T T A A T T C A G G A C A T C T T C C A C C T T G T T T G G C T T C C A G T T G T A C T G C A A G A C C A G T G T C A G G C A C A T A G G C T G A T T A A T C A G T G G
WI-14580	100 G	C A T T C C C A T C T G T C T T G C A	C C G A C C A A G A T C C C T C C	A G A A T T T T T C C T T T T T A A C A G G A C A A G T A A C A G A T T A C A T C A A A C T T C A G A A C T T C T C A A A T A C C T A G T T A T T A T A C A C A T T C C C A T C T G T C T T G C A G A J G G A G G A T C T T G G T C G G C T T A A C A
WI-8540	73 T	G G C C T G C A T T T T C A G G C A C	G C C C T T C T T T T T C A G G C A C	C C A G C T G G A G G T G G A A T A A A T G C G G C A C C A C A G A A A A A C A C A C A G C T A C A C A C A G C C T G C A T T T G G C T T A T C J G T G C C T G A A A A A A A G G G C C G A C C T C T T G A T A A A G A A T G T C T
WI-8039b	97 T	C ---	---	A A G T A G A A C A C A A T A G A A T G G C T C A A A A A T A T C A G A A T G C A T C A C G C A C A T C A C G A G A A A T A C T G T T T G G T A A A A C T T G T T T C A G T T A A A T A T G T A T C J G T G T C C G T G C A T G T C A T G A T T A A A T A T C C T T C T
WI-8039a	87 T	C ---	---	T A C C A C A G T C A C C C T A A A G A A C C A A A G C T T A G G A C T A G G G A C A C A C C A T G C A G A A A G A G A C A G G G A G A C C A G A C A C T C T G G G T T G A G A T G A T T T A A T G C C G C A G C C G A C A C C C A C A
WI-8044	107 C	A ---	---	C A C A A C A T T C A G A A G T T T T C T G C A T T G T G T C T C T G A T G T C T A A A A A G A T T T G A G C T T T G A C T A T A C G A T T T C C C A C A C T G A A C G C A T T C A T A A G G T T T C C C C J C A J A G T A T G G A T T C T C T G A T G A T T A A T A A G C C C C G A A T T C T G G C T A A A G G C T T C C C A C A T T C A A G A C A T T T G A A G G T T T T C T C C A G T G T G G A C T C T C T G G T T T G C A C A A G A A T G G A A C T T C G G C T G A A T G C T T T C C C A C A C T
WI-8550	32 G	G G G A C A C A T C A A T G C A A C A A G	T T T G T G C T T G A G T T T A C A A A T	C T T A C T A C A T G G G A C A C A T C A A T G C A A C A A G T A J G A J A A T T T G T A A A C T A A G C C A C A A A C T A G T T A A T A A T C A T G G T T A A G G G A C A T T G C C A A A G A G C A A C T G A T G C C T C A G T G A A
WI-8057	87 T	A ---	---	T A T T A G A T A A A A C C C T T T G T C C G A T T C A G G A T G T T T A A T T T G C T C T C T T A A A C T C T G T G A C T T T T C C T G G T T C A A A A G G A C A G T A J A T G G A C A G C A G C A G A G G A T G G G G T C T G A A A A A T G A A T C T T T G T G C A A G G C A C T C T G T G G C C T C A C A A C T G C C C C C C T G T C A G A G G G A T G T G C C T T C C A G C C C T A A A G A C A C T A G G G C T T T C A A T G G A C G G G G T G T T A A G C A G C C A G A T G G T A A G G

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WI-6375	28 A G A A	GGTTATTGCA TATGGAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGAAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGATAAAAGATCTC ACATTTGTAAAGGCACATATGAACAATTTATAGCAAGCACAAAGGCAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[A/G]CAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[A/G]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTTCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAATAAGGTGTAATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[A/G]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T C C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTTCTCTCTTTTACACAACTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCACAACAACACGAAACAGTAAACTCTGAGAGAAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAAATTTACATGGGCCCTATTTATTAAAGGACATTTGTGTAATGTTCCACTTTGTTTAAA [C/T]AATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAAATTTACATGGGCCCTATTTATTAAAGGACATTTGTGTAATGTTCCACTTTGTTT AAACAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACCTAAGAAATGGGAAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATA[A/G]CAGCAATGGATGCTGTGTCAGAACATAGTCCCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAC
WI-6629	75 T C G T C A T A	TCCTTTTCAGAG AATAAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTTCTCTGCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA T/CJACCCAACTTGAAGGTGATTGAACCCAAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACTTATTAAAGGAGAGTACTAGGAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC[C/G]GGCTAATACACTGCAATATTTTA TGTTAGCAATTATAGCTGGTCTGTGTATTAACCAAGAGCGGTATCTGG
WI-6690b	106 C T A G C C A C A G C	CAGACTCTGG	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28	T C A G	AAACACC ATTATTAAGG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACACCACCATTAATAAGGAGAGT/CJACTAGGAAAAACTACCAAAACACAGCATGTGAAAC AGTGGGCACGGTGGTAAAGGGGCACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTAGCAATATATAGCTGGTCTGTGTATACCAAGAGCGGTATCTGG
WI-6770	53	A G A A C A C A C A	CAAACCCCA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTAATGACACAGATCTCCCAAAGTAATCCAAACCCCAAAACATCACA/GJAATTATTTCAT ACTATTATACACTCCAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151	A G A	GCATCTTCCA AAAACAAAGA	CCTTGTAAGT ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTCCAGCAATCAGTAGCACTAATCTTGACCAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTTAGATGAAATTCACATTTAAACATGGTAACCTCCAAGCATTCT TCCAAAACAAAAGAAAT/GJAACATTGGAAATAGTCACCTACAAAGGAC
WI-6761	32	C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG/CJA/CTTCTCTCCAGCTTTTGTGAACAAAAC AATTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTTCCAGGTACAAGTCTC
WI-6844	225	T C ---		---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGATCATTAATAACAAAGGGTATTTCTCCTTG GTATTTCAATGATGATTATACAATAAACGAAAGTTAGAACTTAAATGCACCCTGATTAATTATG TAACTGGTAATTTGTTTTAAAAGCATAATAATTTGGTCTCTTTCATATAAATGGGAAATTTAA TATTTCTCTGATAGTCTGAGGTT/CJATCATTTATGAGTAGTGCAAAAGTGTG
WI-6824	112	A G ---		---	CGGTTTTGCTACACTTAATGGTTTTTTTTTAAGGGATTTTTTTCAGGCTTTGTCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTCTGCCAA/GJ/CACCTTAGAAAAATTACAT GACACGGAGAAATGCGCTCTTGTCTTGAAGAGCTTACAGCTAGGGATTTGACAACTCACAGT CTTAGGAAGTGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139	T C A A T T C	GAAAAATGAG ATGCAGTTAA	TCACTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGGCCAACATGGAAGTGTCAAGAAACATCTGTATAGGTACGGACAA AAGAGCTCCTCAATCAAGAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATCT/CJAGAATAATTAAGGCCACAAAGTGAAACTGTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216	T C ---		---	TCCCCAGCTCATATTTATTTGGGCACAGAGTGGCACTCAAATATCTGTGAACCTGAACTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGAGAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTTGCTTCCCAAGGAATGTGTTCTAAATTTGGTTTCAAGACACACTGGTTCC CACTTTTACCACCTT/CJ/CATGACATTGGACAATAGTACTACTCTTTTCTAC
WI-9413	112	G C ---		---	GCCAGTCTCTAGTAAGTCTTAGGGACATGACCAGACAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCATACTTGGGTGGAGGATACCGCTGTATTTCCAGAT/GC/JAAGATTTGGTGGAGGAG ACCATGACAGATGACAAACGGAAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74	C T ---		---	AAAAGCTTTAAAAAAGAGTGGTGTATCTTTAGAAACACTTTTCAGCAAGATCAAGTAGCCACGCT ACAGCCCT/CJ/JGGTGATCTTAACCCCTCTCCTTTT

WI-9617	37 G T ---				TGCTCTTTTATTTACAGTTTCACAACACACGCCGTG/G/TJGGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGTCTCATTCGTCTGTCATGACTGATTGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGCACTCTGTGGCAGAGAGGTGAGCCCTTGCCACACTGGCACC AAGAGTTGCACGATGCAGCTTGAGTGGGTCCAAAGCGGGTGTGCTGTG
WI-9657	121 T G ---				AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTTGCTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAGT/GJATAATCTTT TGATTAATAATAATGTTTATAAATGTTTATGAAGCTCATTACATTTATCTTTTTTAAAAAGTAAAA TTTTAGAACATATGACGCTTTTCATAAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114 G C GCTGGGA			AAAAATTAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT/GJACACCACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTGCCCCGTCTCAAAAAACAAACCAACTAAC
WI-13119a	51 C G ---				CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT/GJACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTTAAATTTTGTAAAGATAGGGTCTCACTATGTGCCCCGTCTCAAAAAACAAACCAACTAA C
WI-13112	71 C T AGCTTTT			TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTTAGGATCATATAAGACTACAGACTTAAGCTT TTTT/C/TCTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACACTATGCGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36 C A CTCAGTACAA			CAAAGTGTA CTACTGATGCT GTTT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA/C/AJAAACAGCATCAGTAGGTACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTGAGAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-13020a	108 G A CTTT			CTAATAGTGG AACCCGTGAGA CTTT	TGCTATTTCATGACAGACGTGAGACAAATATTCITATTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAAACCCTGAGACTTTA/GJATCTGCAAGGGGTTTAATAAT GCAAATATCACATATATTTCCATTTTAAACACCATATTTAAGTTTCCATTTCTTAATAGAAAAATGA TAAAAATGTTTCCCAATAT
WI-12837	87 A G AAAGTCCA			CCATATACAT ATATCAAGGT GCCATAGGAA ATGCTGTTTTT	TGTATAAANAATCCAACTTGTTCCCAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA/GJITACAAAAAAGCAGCATTTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAGCA AGTTGTGCTCA

L42611b	50 G C ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCCTGTG[C/G]CTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACCTTCTCTCTGCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGATGATTTCAACCA CTGGAGCTTCACCTTTGTTAC
L42611	34 T C ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTT[C/G]CTCAGGTTGCCCTGTGCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACCTTCTCTGCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGATGATTTCAACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAGAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ---			TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAGAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTTCAG AAATGTAAGTGTGCCCTCAACTGTTCTTTACCCACTTAATTTCTGCAATTTTGAAGAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTAACACATGG CCTGGTG
WI-1231b	141 G A ---			TCCATGGTTGGTTGCTACTGACTTGTGTAGCCCTTACTGCCCACTATGCATTGGAACATTCOCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTCCTCTCTTTCATTAAATTTCTT TCAQ[G/A]TTATTCCTCACCCCTGAACGCCCTTCTCTCGTAGTGACATTTTAAATCCACCTTTAC ACATTCGGACC
WI-1231a	126 T C A	GGCTCTTTAT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTGGTTGCTACTGACTTGTGTAGCCCTTACTGCCCACTATGCATTGGAACATTCOCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTCCTCTCTTTCATTAAATTTT CTTTCACGTTATTCCTCACCCCTGAACGCCCTTCTCTCGTAGTGACATTTTAAATCCACCTTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTTCCTT TCCAGGCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG T TACTCTATTT TGTTCT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTACTCTATTTGTTC[CT]AGCCACCTGTGGCATTTC CAAAATATGATAATCTCGCCACCATCTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCAGCAGCAG AGTACCTTTCT AACT	CCTTCCAAOCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTT[C]ATAAGATTGTGTAGAGGTTGGAAAGGAGGACAGGA CTGTCTGTGGTATAATGACCCTGTGTCCAGTTAATCCA
WI-601b	112 T A	---	---	TCACCTATCTCTTTTTGTGGTGAGAACACCTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCATTGACTCTCTAACTGAGTACT[A]CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACCTATCTCTTTTTGTGGTGAGAACACCTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAG[C]TGAACAGAGAGGTTTCATTGACTCTCTAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAAACAGACACCCCTCGGCTTCTCTACCAGTCCACATGGGTGCCAAACAATCCCACATTCCCT ACATCTCCCACTGGCTGCCTCTTCAACAACCTCACCA[AG]ACTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTATTGCAACATGGTGTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTAAT	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTTAATCAACCTAGCCG[AG]GCTGTCTATGTGGATTAGAATAAAATA AACACAAAAATGAAACACACACGATTGCTAACAAAGCAGATTCTTTTTTCAAGGCACACGTAAGAT AATAACTTCAA
WI-991	37 A T	---	---	TGCATTCTATTGCACCAATAAATCACTCTGTACAT[AT]CATTATTGTATTTCAATTATCACAAAAT TATGAGTGAGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTGCAATCCATCAACTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAAACACTGACTCTTTTCTCTTTGAAAAACAAGG
WI-1011	70 G C	CAGTATCTGA AGTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATCTGTTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCC A[G/C]AGAAGTCATTTTGTAGGTGTTCTCTGGCGTTTTTGTCTAGCTTTCCTATTTCTCTAATACACTGC CGTCTAAGGGAGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTCTGCACTTCTGTGCACTGAAG
WI-5381	178 A T	---	---	TTCAATGCAAGGTCCTCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTTGCTCATGAAAATTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTGT[AT]TTTACTAAACACAAATGT TTAACTTGGGGTCCACAAACAAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5791b	76 G A	---	---	CTATGTATTCATCTAGCAAAAAGCAAGACTATTTGGATAAGTTTCAAAAAGATGAGAACAGGTCCTA GAACCTCAG[G/AT]CGAAAGGAAGTTTCATCTAGTCCATAGACCTCTATCTCACTGACCCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGGCACCCCTGTTTGT TAGGAA

WI-5791a	44	C G	---	---	CTATGTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTC/GJACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTGCCACCCTGTTTGT TAGGAA
WI-5406c	120	C T	---	---	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/CJCTATGAGCCCCAC ACTTCTCATTTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGAGAGAGGCAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/CJCTATGAGCCCCAC ACTTCTCATTTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGAGAGAGGCAA GG
WI-5406a	42	A G	---	---	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGGAGCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGCCCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCCCAC ACTTCTCATTTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGAGAGAGGCAA GG
WI-5798	48	G C T G	TTTATTCCTCC TTGTTTCTTT	ACTGTTAGAAA ACCAATATTT TCAAT	CCATTCCTTCCTCCCTCCCTTTATCTCCCTGTTTCTTTTG/GC/JATTGAAAAATACTGGTT TTCTAACAGTGTCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T A T T T	TCTTCATGAAT TCATCTTTCAG	GGACTAATTC A TGATCCGATCT	CCTGCTAATAATAATTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT/AJTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCACAGAGAAAAATCCAAGAG/CJCTTAAACCATAATTTTGTGTTTA GAACTCCTGTGCCAACCCACTCTTGATGTGAGTGAC
WI-5481b	131	A G C T G C A G T C G	TGTCATTTATG CTGCAGTCG	TTACTCCAGG CTCCAAGTATT	AAGCCAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG/A/GJA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29	G A A A T T T	CCAAATTCAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT	AAGCCAATTCACATTAGTTGATGAATTTG/AJAATTTACAGTATCTAATGCATGGCATCTGTTTTC AACTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38	T C	---	---	TCATGAGTCTTCTTCAAGATGCTTGTAAAGTCCCAAT/CJCAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATAATTTGCAGACCAA

WI-5826	134	T C	---	CCCAATACTTT TTCAGGTGAA	---	TATTTTTTTTCTCAATTCTGGAGCACACCATGCTCTTTCTATTCTCATGCTTCACATTATTTTTT TTTCACTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATCTTTAGT[C] TTTCAAATTAAATGCCACATAGAAATAATTTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCCT CCTGGTGCATTTACTCTTTACAC
WI-5546	40	C T A	GGCACCAGCCT TTTTAGAGT	CCTGTATTTTA GCAACATGGG	CCTATAACCCCAATACTTTTTCAGGTGAAAAAGGGGAAA[C]/TACCCATGTTTGCTTAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAATCTGATGTGGGAATAT TAGAAAATTAAAGCGAGAGAGGCA	
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG OCCAGG	TGTTTGTTCTGCACCTCCCCAACAAAGTGGTCAATGAGCCTCAAGGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCAGCCTTTTAGAGT[C]/TCTGGCAATTTGTGCACTAGTGTACGA	
WI-5836b	161	C T	---	---	ATG	TAAGTTGATTTAAACACTCTGTGCCTCAATTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAAGTGGATAGACATGAATACTCTGATGATACTGTTGTATCCCTGAA TCTGCAATATACACATGATTCAATGAT[C]/TCCATTTTGAAAAATTAAAGCTTTTGAATTGTTTTTCCA
WI-5573	58	C T	GTTCATAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATCGCTTCACCCTCGATGATGCGGCTTCATAAGGAGGTGGGGA[C]/TGCACAC ATTACTCTCCAACGTTCATCAGAACACTTCAACAGCG	
WI-5850b	134	G A	---	---	---	CAGGACCTGGAGCCTTTGCTGTTTGCTCTCCACCCCTCACTCTTTCTCGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATATGCACGGCTCTATCTTATATGGGCAATATCCAATGTCCCATT[C]/A TTTTGCCATTTCCGTATATCAAAACAGAGAAGCAGAGGGTGG
WI-5850a	92	C T	---	---	---	CAGGACCTGGAGCCTTTGCTGTTTGCTCTCCACCCCTCACTCTTTCTCGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCCCTATATGCA[C]/TGGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCTG TTTTGCCATTTCTGTATATCAACAGAGAAGCAGAGGGTGG
WI-5612b	125	A T	CTATTAATGA GCATCGTGTCA TTC	TTCTCTTGAGA AACCTAAAAC ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTTAACATCACAATATCTTATTCTGCGCTG TCACACTAAATTGCAAAGCATTCAAATTGATTGACTATTAAATGAGCATCGTGTCTT[C]/T/CAGTGT TTAGGTTTCTCAAGAGAATTATGCTGTCTTCTGTAACTCAAGTA	
WI-5612a	44	T A	---	---	---	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTTAACAT[A]/CACAATAATCTTATTCTGCG CTGTACACTAATTGCAAAGCATTCAAATTGATTGACTATTAAATGAGCATCGTGTCTTCAACAGTGT TTAGGTTTCTCAAGAGAATTATGCTGTCTTCTGTAACTCAAGTA
WI-5636	26	A C	GCCAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA	TGAGAGCCAATTTTATCGGCAATAAA[A]/CTTCCCAAAGTCTCTCGATGGAGGCATTTTCAGAAATCGGG GCAGGGGAGCGAGAAGGTGAGACAGATGTGAAGAAC	

WI-5865c	103	C G ---			---	TTAGAAACCTCCATTTATCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTCTCTATCAAAAATAAA[C/G]AAATATTAAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACCTAAATAATTCAGG
WI-5865b	99	T A ---			---	TTAGAAACCTCCATTTATCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTCTCTATCAAAAAT[TA/AA]CAAAATATTAAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACCTAAATAATTCAGG
WI-5865	165	T A ---			---	TTAGAAACCTCCATTTATCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTCTCTATCAAAAATTAACAAATATTAAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGT[TA/CC]AGTCTCCATCTTCAAAAGGTCACAGTCCCTC AGAGAAGACAGACAACCTAAATAATTCAGG
WI-5874	76	T G	CATAGCATGG ATAATATTAT ACAGAAAAA	CCTAGTAAGTT TCAGTCAATTG ATATGT		CTCAGACATTCATTTTCAATTAGTTGTTAATTTTGTGTAATTTTCATAGCATGGATAATATTACAGAA AAAAAATTT[GT]ACATATCAATGACTGAACTTACTAGGTAGCAATTTGTTTGTCAATTTGCT
WI-5752	36	A T	CAGCCTCTCAG TTTTTCCATC	GACAGAAAAAG AGAGTAAATT ATGAAAAA		CATGGAGCCGACGTTCCAGCTCTCAGTTTTCATG[A/T]TTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTCGTATTTCAACTCTCATTTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAAAGTAAATG
WI-5760b	61	C G ---			---	TTAGCAGAAACAACAAAAAATGTCACAACACTGCAGTAAAGAAGTGTTCCTCCGATAAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAAACGAAGCCGAGTTTCGATTTCACACA GTTGCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAAAACGAAGCCAGTTTCCGATTTCACACAGTTAGTTGCTGTT
WI-5760	187	G A ---			---	TTAGCAGAAACAACAAAAAATGTCACAACACTGCAGTAAAGAAGTGTTCCTCCGATAAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAAACGAAGCCGAGTTTCGATTTCACACAGTT GTCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAAA ACATTGTTGAAAAACGAAGCCAGTTTCCGATTTCACACAGTTAGTTGCTGTT
WI-5944	52	A G	TTCTCACCATG GGAATCTTG	GGGTGGGATCT AATCTGCA		AATATCTGGCTTTTCTCTTAGGAGGAGATTCTCACCATTGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGTGAAGACTACTCTCAGTCTTCTCTGCTG
WI-5967b	148	C T ---			---	GAGTTTAATGAATCCTGTTCCCTCTCTAAAAACCTCTGTTCCCACTTCCATTTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCTGTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGT[A/C]TTTGTCTGTGCGGTATCTGCTCCAATCACCCATTCCACTTTATTTCTCTATTAT GCTGAATGAAACGGTTATATTACAG

WI-5967	165	C T ---				GAGTTTAAATCCTGTTCCCTCCTAAACCCCTCCTGTTCCCCCAACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGGTGTGAG TAATGCTTGGTACTTGCTCTGTGCCGTATC/TTJGCTCCAATCACCCATTCCACTTTATTTTCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53	G C ---				GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAAATG ATCTGACTTCTCCAGAACCCCTCTTCTCTGGAAGTCCAACTGTGCACCTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAACTTGATTGACGGGTGAC ACACCATGCTTCGAGAAAGGAATGAGG
WI-6141	80	T C AGGTACTT	CTTCTTAATTA AGCATCTACA		TGAAACCCCA GAACAGTG	GACTGTCTCAAGAAAAAATAATGAATAATTGAATTAATTAAAGCACCTTCTTAATTAAGCAT CTACAAGGTACTTAT/C/CACCTGTTCTGGGTTTCAATCCTCTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAAAATTTGTCTTTT CTC
WI-6450	45	T G TGTACA	CCAATGACTT ATTCTATATCT		TTGTTTGAAT GTGTTGACTT CT	ATAGGACAGTTTTTCTTCCAATGACTTATTCTATATCTTGTACA/T/GJAGAAGTACACACATTTCA AACAGAGCCAGGCTATGCCAGGGTGGATTATTTTCACGGTCATGGTAATATGCATGTAAAGACTA TTTTACTGGCTTCTTTTATGCATAAAACAGGATTGTTCTATTCAACAAACATGTGTCAATACAG CAGTTGTCATGTCCCTCTGGTACTAGATATAGTCTTTATAGAATATGTGGTTTAGAATAAAGCCACA AATTATCTATAAACAACA/C/TJAAAGGAACGAGGCTCAAAAGTGAACAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAAAATATAATCCGTGACCTCTTA
WI-6461	88	C T ---			---	GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTTCTGGTCACACAGGGACTTTCTGGGCT ATGAAAATAGTCTATTTCAGTGAACACTAGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT CCTGG/GJAJAATATCTCACAAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
WI-7466c	141	G A TTTGTCTGG	TTTTCACAGTC		AGTCGCATGCC AATTATAAT	GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTTCTGGTCACACAGGGACTTTCTGGGCT ATGAAAATAGTCT/TJATTTCAGTGAACACTAGTTATCATAAAGACATGCAAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCTTT
WI-7466b	80	T C GTC	GACTTTCTGGG CTATGAAATA		ACTGAA	TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTCTGTCTCCATTTGCCACGTCTTCCTC AGTAGAATAAGACAGGGACTTTGCTGGTGTCTATCT/C/JTTCCTTCAGAAAGACACTTGGCCCT CATAGGCATTCATAGATATTGTTGAATGAATGTGCTTTTGGCATATTGATTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104	C A ---			---	CCTCTAACCAAGAAAAACTTGACTTCCTCAACTCAAAATACCCCTTCTCTAATAATTTJ/GJAGTAACCA AAATATTCTTCAAAATAAATTAATCTTTTAAATTAGAAAGAACCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9720b	55	A G ---			---	

WI-9720a	47 A G ---	---	CCTCTAACAGAAACCTTGACTTCCTCAACTCAAAATACCCCTCTCTAGJATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAACACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---	---	CACGCTCTAAGGCAGGATGTGGCTTATGAGATACTTTGCAATGTCTGTGACACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTCTTATJGAGGATTAG TAAGATCTCTTTCTAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTAGTTTGCAAT TAAGAAITGCCAGTCTTTTGCTGCATCATCTTGAACATTAATCCACATG
WI-9748	74 C G ---	---	CCACTTCAGTAAATCAATTTGTAGCACTTATTTCTAAAGATTCTAAATTTTATATGTTTACCCCTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTCTCCTGGAAATCTTTCAGAAT TACAGTTATGATGTCTTTTATATTCCCA
WI-9943	91 T C ---	---	TGAGGCTATGATTGCAGATTTGTAGTGACTAATACTTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTTATATCCATCTT[C/T]CJATTTTAAATTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTTAATATTGCATTTACACACCTTCTCTTTTGTCAATTTAGGGA
WI-9891	39 T C ---	---	AGGGGCTTCACAGATCCGTACAGTCAACACTGCCTCCTT[C/G]JAGTGAGCCTGTGAACCCCAAGAC GGCTGGTCATCAGTGTATCCTCTTCTTCCGGACAACATCTTTAAAGAAAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAAATAATCTTATTAGGCCAAATCCAAAT GTGCTGAAATATCTGCCAAGCATGTCAATCTACACAAAAGGATTGTGAAA
WI-9897b	84 C T ---	---	CTCAGAAATTTACAGATCTCCCCAAATGTCATGATTTCTGTCACACATCCTATTTTCTCCTCAAAC ATTTATCTAGCCTGT[C/T]AAGTCATCCAGTGAGGCTGTTTATCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTTGTACCCACATTAA
WI-9897a	83 A T ---	---	CTCAGAAATTTACAGATCTCCCCAAATGTCATGATTTCTGTCACACATCCTATTTTCTCCTCAAAC ATTTATCTAGCCTGT[C/T]AAGTCATCCAGTGAGGCTGTTTATCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTTGTACCCACATTAA
WI-9935b	115 C A ---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACAC[C/A]JAGCCAAAGAAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9935a	42 C T ---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCA[C/T]ACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACACAGCCAAAGAAAAAGCC TGATATTAAGAGGCACCTTGCAATTA
WI-9983	146 C T ---	---	CCTGTAGGTGCCAGAGTCCATGCTTGGCCACAATGTTAGGCTGCCTCCCCATTTCTTGTCTTGA TTCCCCAAACCCCAAGGTTCTACCCCAATCTGATCAAAATGCTGACTAGGTGCTGGTCAGGGTAA AGCATTATGA[C/T]JAGACACAAAGACAAAGAGGTTAAAGTTGCTGTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T A T C T	TGATGTAATGC TATGTAAGCAA	TGATTACTGT GCTTAGGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTGTTTATTATGTGTGCTATAAATCAATGTTCTTA ACATTCAAATAAGATCTTTTGTCTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTA[A/T]TCCCTTAAGCACAGTAATCAAGGCCTTCTACCCCA
WI-10020b	122	T A T T T	GCGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAATAAGCAGTGTATTTATGGCGAGAAAAGAAATCATGACTTTT[A/A]AAAAATACC AGACTAATGATTAAATAAATTAAACAGTCTAGGGTTCGGAAGTGGCCTAAAGCACGTAAGTAGCCCT CCTTAGA
WI-10020a	39	T C A T A A A T T	TGTCATCTTGA CTCGTATTAA	AAATCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATT[A/T]GTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAATAAGCAGTGTATTTATGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAAATAAATTAAACAGTCTAGGGTTCGGAAGTGGCCTAAAGCACGTAAGTAGCCCT CCTTAGA
WI-10064b	170	C T T T A C A T G	CCTTTAGATAT ATTGTGATTGT	ACCITTCGAA GCCAGATTTC	TCGTAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATAATTGTGGTGACACTCTGTTTATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG[C/T]GAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C A C A G G G A A G G	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCGTAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG[C/A]ATTATAATA AATAATAATTTGCAGAGCATCTCTCTCTATGCACCAGATAATTGTGGTGACACTCTGTTAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T C C A A C T C T T	TCCTCTGTCCC CAAACCTCT	ATTCTGTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCCAAACTCTTA[T/C]TTAATTCATTCAATACAACAAGAATTTATAGAA TATGCACCACATGCCACAAGACACCCCTTATATTAGT
WI-1319	40	A T A T T C T T T	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTTGTGGCACTTAGAACATAGTTTATTCCTTT[A/T]ACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGGTCTCTGTTTATAAATTTGGTATCTTTTGGCCACAAGAGTCTGTCTGAC AGCTTATGATCTCTATTTTAACATTAAACACTGGTTCAGATGTGTTTAAAACTTGTGAACCTGCAGC
WI-10316	104	T C C T C T T	CTGTTGATTTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAAGCATCTATATTACCAGTCACCAACCCCTG GACTATAGTCTGTTGATTTCTACCTCTATTCTCTTA[T/C]TAACTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGCCAGCC
WI-2572	61	C T	AGTGAGTTGTGCACAATTTTGGAGACATTCTGTGACCCCAACTTAAACACTTCTCCACACA[C/T]AC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

WI-10368	31	C T	TGAAGCAACC AGGTCTTGTT	CAAGATATTAT ATTTATCTCT AAGAGGGG	GAGGAACGCTGAAAGCAACAGGCTTGTTC/TCTACCCCTCTTAGAGAATAAATAATATATCTT GAGATAGGAGGAGCAGCCTGAGGACAGCTGGGTTTTGTTTCTACCCCTGGAAGCAGAATATCC TTCAAAGCTTTTTCCAGTGAGTCATGTTGCTGCTAACTATATGACCCCTGATGGATTGCCCTTTCAGGG T
WI-10391	32	A G	CTGCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCCGTTCTCTGCTCAGGTATGACTCCCA/GTCAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTCCAGGGGACGCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACATTGCAGAAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146	A C	GTTACCCAGA GTCTTCTAATA GCAA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATAATATTCTTTTTTCATATT TTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTTT CTAATAGCAA/CJAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82	A C	GGTGTCTCAAT AAATATTATT CTTT	AAAATCTGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGCTCAATAAATAATATTCTTTTT/CJTCAT ATTTCCAAATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84	C G	CAAACTTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGTCTT C	CGTTGGGAATATTTCTATCTCACCTAAATATG/C/AGTGATTAATAATACATTTTAACAAACTTCAA TTGCTTTAAGTACTTTA/C/G/AGAGACCTTGACTGTTGGATTTTTCGATTTTCTTTATTTCTTAATA AAACATGCATATTTAAGTTGTGACGCAAGATGACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33	C A	GGGAATATTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATATG/C/AGTGATTAATAATACATTTTAACAAACTTCAA AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTTCGATTTTCTTTATTTCTTAATA AAACATGCATATTTAAGTTGTGACGCAAGATGACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125	T C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAAAACCACGCTTAATCACAATCACTTTTCTTTCTGTGTA GAGCTCAAACTCAGTCTGAATGAAATTTGCTGCACAAATGTAAACAGAATTGATCCTA/T/C/ACTGGG ACTACAGCCATGGAGAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58	C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACAAAAAGTTTACCACAGTGAATTTATGACCAAAATGAGA/C/T/AAAT TTGTAAAAAAAACCTCAATGAAGAGACAAAATATAGTTCAAAGATTGAGTTCAATATTGT ACCTACAAAATAGGGATAGTCATGGTGTGTCAGACATTTCTTTTCTTTTCTTTTGT/G/C/CTTTA GAATCCATTTTGTCTTTTGGCCAGCATCCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTCCCAATCCAGAGGCGGACTATTACCCCATGGGGTGCAT AGAGAGGATTAAACAGGGTGATGCTGCAATGGGAATATTGAAAAACC
WI-10656	59	T G	---	---	---

WI-11169b	154	T G T T T T	T T A A C C A A G A G T T T T C A T T C	C T A A C T T A A A A A T C C T C A T T C A A A A T A T A A	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T T C T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A A T T A A G C C T A A A G T A G T G C T T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A A G A G C A G A C A [T/G] T T T A T C A T G T G T T C T G A T A A T T T T T A T A T T T T G A A T G A G G A T T T T T A A G T T A G C A T
WI-11169a	95	A G T T G A A A A A	A A T A A G T G A A A G T A A C T G A C	A A A C T C T T G G T T A A A A A G C A C T A C T T	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T T T C T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A A T T A A G C C T [A/G] A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A A G A G A C A G A C A T T T A T C A T G T T C T G A T A A T T T T T T A T A T T T T G A A T G A G G A T T T T A A G T T A G C A T
WI-10685	25	A G ---	---	---	C A A G T C T T G G A C C T T G G A T A G G T C [A/G] A C C G G C T G A A G G T T G G A C A G T T G T T G T T A G G T T G G A G A C C A A A A T T C A G T C A T C C T G T A A T A T A G A T C T T G T C C T T T T G G G T T A C C A C T A G G G G T C A C T A A A G A G A T G G G A G A C A G T C A A T C T T G T C T A A A T A A T T C C A A A A T A G C C A T G G G T T G G A C A A A A T A C A A G G T A G T G T C T C T A A C T T T A A T G G G C A T A
WI-10686	133	C T A A G G	T G C C C T G T O C T A A G G	C A A T C T A A A T T C A T G T G T A G A C A C A	A A T A A C C T G T G G C A C A T A A G C A A A T A C T G A G C C C A T A C A G A G T G T T T A T G T T A A T A T A T G A A A A A A G T C A A G A G A C A A G A T A T A G T T C T G C T A G A A T A C T T G A A A T C T G A T G C C C T G T C C A A G G [C/T] T T G T G T C T A C A C A T G A A T T T A G A G A T T G A A T G A A A T G G C A A A T T C A G A A A A G G G
WI-11175	77	T A A	A A A T G A T T C T T T C T G C T C A A A G	C T G T T C T C A C A T T C T T T T T G A A A A	G G T A G G A T G A T T C T A G A A T G C C A C T T T A C A G C C A C T G A A A T A T A T T G C C T C C C A A A T G A T T C T T T C T G C T C A A A G A G [T/A] T T T T T T A A G T T A T C T A C T A T T A T A T T C T G C T T T T T C A A A A A G A A T G T G A G A A C A G T A C A A A A T G T T C A G T A T A G C A A A T T A A A A T T A A T T A A A A G T A A G A A A A A A G A A G C C A A T T T G G G C
WI-10694	144	A G T A T G A G T T T C	T G C A A A T G C T T T A T G A G T T T C	G G C A T T T T G T A A A G G A G G A A A	T A G A G A G G T C T T C A G T T C A G G T T G G A G G G T G G T G A G G T G A G A T T C A C T T C T T A G A A G C A C T G G C T A T G T A C A G A A A G A T A A A C T C T G A G A A G A A C T C A G T T C T A A A G T G T C A G T C T T T G C A A A T G C T T T A T G A G T T T T C [A/G] T T T C C T C C T T T A C A A A A T G C C A T C A A T T C C T C A A G G A A A A A A A A A A A A G C T T T C T T
WI-2716	23	T C C	T G A A T T C A T C C A G A A A A A C A G	T C T C T T T T C T C T C T T G T T G T C A T T C	G T G A A T T C A T C C A G A A A A C A G C [T/C] G A A T G A C A A C A A G A G A G A A A A A G A G A A T A A A G G T T T T T G T A T A C G A C A A G T G G C T C A A G C A A T T T T C T G T C C C A G T G C A T G G A G C A G T G
WI-10719	115	T C G C C A T T C T A G	T G A C T C T C A A G G C C A T T C T A G	G C A C T G C C A G C A G C C	C A G G C C C A A C T C T G T C A T T A A G T G T T T A G A A C A G A C A C C T C A G T C A C A C A A A G T T T C T T G T A T G T G C C C A C C A T A A C A G T T A C T G G A G G A T G A C T C T C A A G G C C A T T C T A G [T/C] G G C T G C T G G C A G T G C T T T T C C A G C C T G C T G C C C A T A A C T A A
WI-10721	40	A G C T T G C C A	T G G C T C T G C T A C T T G C C A	G A A C T C C C A C A T A A A T A A A T C T C A	C A A C C A A T T C A G A T T A A T T T T T G G C T C T G C T A C T T G C C A [A/G] A T G A G A T T A T T A T G T G G G A G T T T C T G A A G A T T C C C A T G G T A A A T A G A T A T C C T C T C C C T G C T A G G T T T T G A A G A A G T T G A A

WI-11204b	88 T C ---	---	---	GCACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAGAAAAAATTTTCCACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTTCAGAAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAAA TACCTTT	TGATCACITTA AATGTACATAA	GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAGAAAAAATTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTTCAGAAAG GCAACATC
WI-10732	80 C A ATTGGTTCACT	GCTGTGCTTC	AAGAACAATG CATAACAGAA CTTTAA	ACATGTAATTCCTTTAGTGGTCAAGCTTCCTACCCCAAGAATATCCCTGGTTTATTGCTGTCTTC ATTGGTTCACT/CJATTTAAAGTTCTGTTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACCTCTGTTAAACTGTC
WI-11206	127 A T ACTC	GGTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGCTTTTCTTTGTACGAGTGTATATAAGAAATACCACCTCTGTACATTTTGTAAAAAGATAGCACAG AGAGAAGCATTAACAGGGCACAGCAACACATGAGGTGTTGTTTCTGTATGTACAACTC/ATJCCAA CCATTAGGAATGTCACTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATTCACACATGGA ATAAGTCTA
WI-11215	68 C T ---	---	---	GAAAAAAAAGTTTTAATTGGATTGCTTAGTTGCTTAAATTTGACCTACTTTCAGATTTATTTTAGT [C/J]ATTTTCTATAATATTTCTTGTAAGTGATGGATTTCTATAAATTAAGGAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTTATCCAAAGCCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATGAGAGAATAATCCAAAAAGTAGAGAAAAA GAGACAAAAGAGATGAAAAATAGGA[G/A]AGAAAAGTGTAGAAAAATAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ---	---	---	ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATGAGAGAATAATCCAAAAAGTAGAGAA AAAGAGACAAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GGCTGG	CATACCACTGC	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGGAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCACTGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGGCTG G[G/A]TCACAACCTTGGCTACCAGGAGAACCTTGACACAGACTTCGTAATTCGTTTCACAGGCTACTGG AAAGCC

WI-1122a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTTGG	AGCCACAGTGGAAATCATTTACACTA/C/TJCGAAATCAGCAAATGCTAAAAATGGGGCTTTGGATTTT TGTTTTTGTTTTTCCATAGACCCACCCTGGTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTCAACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATGCTTTTCACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTTTTATGCCATATTAAATTCATTACACTC/TJACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGGATATTCCTGGCAGCATAATCATTTGTTATCATTAGACATTGCA GGAACCATATGGATGGATAAATGTGTTGTTTAAIGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAAATTAATAATCTTCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAAGAAATTTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/[A/C]GACATAGTTGCTAAGGATATTCACACAAATAT TTCATGA
WI-11226	165 A C ---	GCAAGGGAGG AACATTTACA	---	CAGTGGCTGGCTACTGACAAAACGTAAACATCGTGGAGGTGGCAAGGGAGGAACATTTACAG/[A/G]G TCCATCTCTGATGTACACAGCGGCCAGGAAGGTTGATCTGGAG TGGGACACACTGCTCTAGACC/[T]TCCCAGGGTCCCTCAAAGTGGGTGAGAGGCCCTACTGCCCT GCCCTGGGACGCAGAGGCATCAGGGCCTTAGTCTCTCTGGGACAGTGAAGGGCCACCACC ACAGAAAAATGCCTAGGCTTTGTAGCAAGAGAGGAAAGCATCTTCTATGGGCAAGAAATTC/TJCATTT CTGTGTTTCTTAGGTTTGTTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGTATCCAGCAACATT TCCGTAACCTACCTCTAGAAAGTCATGCAAGAGAAATGATGA
WI-10778	62 A G	AGAGATGGAC	CTGGTGACATC AGAGATGGAC	GGACAAAACAGAAATTAATCTGGCA/TJAGGGTTTCTTAAACATTTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGCTATAATATTTGGATACATTAGGCTCATTTAGAAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10789	21 C T GCTCTAGACC	GGGACACACT	TTGAGGGACCC TGGGA	TATGCCCTCCCAACGAGCCATCCACGCTGCTTAGCACAAAAAATAGAAATACATCATTTCTGAATG GGCACAATTAATCTGCAGGCTCTCC/[G/C]TTTCTAAGTCACCTGCAGTTAGGCTGCAGACACTGTGTA TACCATATAATCTGATTTCTGAGCAGGAGGGGAGGCAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTCCG
WI-10828	23 T C ---	CATTAATCTGC AGGCTCTCC	A	GATTTGAGTATTATCAAAATTTGCCAAAGACCATTAAACAGATTTAATAGTTAAAGCCAAACTATA AAGAAATTAACCTGTTCAAAAGTGTTAAAT/[C/T]CTTAATACCAATTTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT GGATGATGTTCTGTGGTCCCTTAT/[C]AAAGCCTCTTGCAATCCCAATGTGTAAATTTATTTATCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCC
WI-10832	91 G C	AGGCTCTCC	AGGCTCTCC	AGGCTCTCC
WI-10834	96 C T GTGTTAAT	AGGCTCTCC	AGGCTCTCC	AGGCTCTCC
WI-2287	24 T C ---	AGGCTCTCC	AGGCTCTCC	AGGCTCTCC

WI-2296	81	A	G	TGTTACTTTGA TTCCTTGCTCT	GCAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGTCTCAGGCTTTAGAAATAAGTTGTTACTTTGA TTCCTTGCTCTGACAGGCTCAGTTAGCTGTGATTTGCAGAAGGTTACATTTGTTGTTG
WI-2300	77	G	T	GGACACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCCCTTATTTAGCGGGGCGAGGTGGTAGGCACAGAAGC CAGTCATACGTTTGCCTTAAATTTGACCAACCATTAAGAAATAGCATTTCA
WI-2371	55	G	T	GTCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGTCTGGTCTTGTCTTCCAGCTTCTGTTGGTGGCT GTCAATCTTTGACATTTCTTGTCTTGCAGCTGTATAATCCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCGTGTCTGTG
WI-2395	122	A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTTAAAGATAACATAGAAATATCATAATACTTGGTTTAC TGAAATCTGAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTTACTATCCAAATGCTGAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTAAGAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCCA
WI-2437c	192	G	A	---	---	CACGAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179	G	A	---	---	CACGAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128	G	A	---	---	CACGAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTCTAAATAATAGACACCAAAAAATTTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71	G	A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTCTTCTCCTTAGACCCCTCCAGAAAAATATGCAACCTACTGACAAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123	T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGTTTACAACCT GTACCACAAACAT G	CTGTAACTACACACATCCTCCTGTAACTCTAGGTTACTTGTAAATACAAAAACACAATGTAAATGCT ACATAAAATATTGTCACTATATTGTTTAGGAAATAATGACAAGAAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAAACAGCCATTTTCCCAATATTTTCAATCCACAGTTGTTTAAATCCACAG AAACCACGAATG
WI-2886	46	C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAGA[C/A]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTCAAGAAAAACAGAGGAGCGTT

WI-2906b	77 T A ---			CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTTGCTGGAACCTTGCTGGAATGCTCTTTCCCTCTT/A/GAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTGCTGACCAACAAA
WI-2906a	50 A C TCTTGCTGG	GACACCTTCAT	AGAGCATTCCA	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTTGCTGG[A/C]ACTTTGCCCTGGAAATGCTCTTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTGCTGACCAACAAA
WI-1736	175 C T ---			TACTCCTCATCTCTCATGTCCTAGACGTAAGCTCAGATTTCCATGCCCTGAAACATTTATTCCCTAAATAGATTCCCACCCCGAGCACTATTTACACAGAAACAGCATGGAGCAGTTGGAGCTGGCTCTTAGAGAAGCTTACTTAAGGACAGTGTTTTCCATCTGCTTCCA[C/T]AGAGATCTAGGGTGCTTTTGGAACCACTTGG
WI-1851	136 G A GTGTTAAGTA TTG	GCATTGAATT	CACTAGCAATG	AATACCCACGCTCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAACTCTGGGAGGACACAAACATTTAGACCATAGCAATTGAATTAAGTATAGATGTGTTAAGTAAATATATAACATGGTACA[G/A]ACAACCTCAGTTTAACATTGCTAGTGATTCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62 G A AGAGACCCC	CCCAAAACAC	ATTGACTAAGA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTGAGCACCCCAACACAGAGACCCCG[A/T]GAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGGCTGGTCATAGTAGACACT
WI-1754	177 G A TAGTC	TTTCTCCCTT	AAAGTCGAATT	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTTCTCTTTCTGTTTTGTTTTCTCCCTCTTAAAGAGATAGTC[G/A]CCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A TAGATT C	AAATTCACCC	TGTGATAGTTT	ACAACACAGCAAAATTCACCCACAGATCTATTAGATTCTT/A]CACCCCATCTCAAAAATCATCATCAAAGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140 G A AGATAAAGA	GTGGAGTGGGC	TCACTCAAACT	CAAGCACACATTCAGGCAGTGGCAGGTAGGGAAGGTGGGCAACTTGGCGACGAGAGAGGGAAGAAGTTTCAGACCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGCAGATAAAGA[G/A]CCAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAAG
WI-1775	47 C T TTTTCTCTG	CCTGCATGGTC	ATGACAATGAT	ACTCCACCACACAGTTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTCTG[C/T]TTTACATCATTTGTGATAATCTCACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A ACAT	AGCATATTCA	GAGGACTTAA	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCCTTACAT[G/A]CAAAATGCTCTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCTTAGGA

WI-3416	33 C T	CAAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCTCAAGTTGTAGCATTCAGAAGTC[C/T]CTCTTAGAGGTAGTTGTGCTCGTCTGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCCAAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGCACAACAATAATTAATCCCATTTGCCATAAAAGACCAGG
WI-3453	70 C T	TTCTTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAACAACAGAAATTTAACAAATTTGAAAAATCAGCTACTCTTCTTAGGCCCATCAGAG AATC/TGAAGTCATGGGAAAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCAC[A/G]GTATTTAATGAGGTGGTGTGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTAGC AC	CAACCATCAAT TTTCICCCA	TTTGACCCCATACATGAGAAATAAACCCATAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTTGGG TTTCTGGATGTCT[C/T]TGAGGACAGGGTCACCCAC
WI-3502	79 C T	CCTGGGTTTCT GGATGTCT	GGGTGACCTG TCCTCA	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT[G/C]ATGGAAAGGCTGCACCTGGATGAGGTCACAAA
WI-3600b	146 G C	CCATGCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGT[G/G]GAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTACAAGGTAATCCACTACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTACTGTGCTGTTATGATGCACCT[G/T]CCTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAAGACACAATTTACCTTGTGTTTCAGGCGCAAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTTCCAAAAGCCTTTATGCTTAC
WI-3678	125 G T	---	---	AAAGCGATGTTGAGATCCACATTCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T[A/C]AAAAACTACTATAGTTTATGAAAAATGACTTCCAAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAATCCAGAATACTCTCTGTCATTCCTTAACCTTGACTGCACAG
WI-3687	67 A C	---	---	TCTAAAATGTGAACCCAAAGAAATCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAATGA AAAAC[T/C]ACACCCGGTTCAATGAAAAACAATGATTGGTGAGCCATGTCCTTATTTAATGAAAA GATCTGGGCAATTAACCTG
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA AAAC	GGCTCACCAT CATGTGTTT	

WI-1819	51	C T	---				GAAAAGCAGGAAGCCAGGACAAACTTTTGAAAAAGTCTTTGAGCAC[C/T]TTCGTGGATCCG AATTTTAGTGTGATTTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAATTGC CAGATTAGCGATTGTTTGACTTGTTCCAAATTAATGAAATGTGGAAAAAAGGGTGGTAACGTGT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116	G A	---				GGCCTATTACATGACACTGGGCCAAGATCTTGCTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C	CAA	ACAGTCATTT AGTCTTCCCTGA	TAAGATAACC ATACTAGGTAC	ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACACAGT CATTAAGTGGAGAAGCCAGCAATTCATCAAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C	G	TGACCAATGTC TTTAGAAGCA	TCGTGCGTGTG CTCTCC		CAATGACCAATGTCTTTAGAAGCAG[A/C]GAGAGGACACCCAGACACACACAGGAAGGAGTGAG GTGAAGATGAAAGCAGTGTGACGCAAGCACAAGGTGAGGAAGCAAGGGTGTCTGGCCACT
WI-3901	114	A G	---				GGACCATGTCCCTCAGAAATACATTCAAGCCCTGGACGGTGTCTTAACTGACACTGTGACCTCAGGCA AGTCATGTCTGCTTCCCTGAACCTCGGCTTCCCTCACCTGACAAGTGG[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	C T	GC	TGATTCTTCTG AAGACTCACA	TCTAGAAGCAA TGAAGGATGG		CTGAGGAGATTGATGCTACTTTACCTGAGGAACCTTTTATTACCTCCCTGAGTTTGTTCCTTGCAA GACATTGCTGATCTTCTCAAGACTCACAGC[C/T]ACCATCCTTATTGCTTCTAGACCTATAACTAG ACTCAAGTCCCGCAGCAGGCCCTTAAAGGTAAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA	ATG	CCACTCCCAGGCCAAAGAGCGTCTCTATGAATCAT[G/A]CATTTGTTCTCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAGGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAAGGTC
WI-4091	84	A T	GTCATTGCATG	TTGAGGTCTTA GTCATTGCATG	TGAGTTCCCTAT TAAGTGACAAT	ATTGTT	TAATTCACATTGCTCTTGTGTCATTTATTGCTTCTTATGTAAACACAATCACCACACATTGAGG TCTTAGTCAATTGCATG[A/T]GTATAACAATAATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CAACAGAA	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT	AGCC	TCCTCTCTGTAATAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGGTGGCTTCTAAGATGGTAAT ATCTGTCCAAAGTTTTGTTCTCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G	AAACA	GGTGAGAGTC AAATTGATAG	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCTGCGATATACCTTCCAAATGACTAGTATGAATAAGCACGTATTAATTTACCTATTATTT AT/CJCATCATGATTTGCTGCTTCTTCCAAATTTACTACAAATTTGATTGTCACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24 C T	CTGTCACTGGT CTGCCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCCCTG[C/TTGGTCTGTTCCCTGTTCTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTGGGCAT
WI-4250b	117 A G	---	---	TAAGTGCAATTAAGTGTACAAGTCCACAATACTCTTCCACCAAGTGTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTTGTGAACAGGGGTGGGAAGGATCCTGTAAAGG[A/G]TAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAAC AGG	CTTTTACAGGA TCTTCCCAC	TAAGTGCAATTAAGTGTACAAGTCCACAATACTCTTCCACCAAGTGTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTTGTGAACAGG[G/TTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G C	TGCTCCCCCAT CACCT	G	TAAATGCTCTGGGAGATAATAGGAAGGTCCATCCTCTGATACCTTGGTTGCTCCCCCATCACCT [G/C]CCTTACACAACCTGAAGTAGGCCCATCCAAACACTGTGTCAGAAAGATAACTGTGCGAC
WI-4256	57 C T	---	---	ACAGCCTCTTCAATGGCACAATCAAAAGCACCACTGTAAGGAGGAGGCAAAATCTGG[C/TTCTCAC CATTGGAAAGTCTTCTGAAGGATAAGGAGTGAATGACTGCTAGAAGAGAATGATTGGCTT
WI-4325b	71 C T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGCTTTTAAATGACTCTTCTTGGTCTTCAAGATATCACCAGCCAC GATG[C/TTTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGCTTTTAAATGACTCTTCTTGGTCTTCAAGATATCACCAGCCAC TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4347	158 A G	---	---	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGTGGGTTAACTGGATGCCACTTCTGCCTGTACCTTCT CTAGACTCTTGACCCCTGCAGGAGGATCCCTGGCTCTGAGTTTATCATCTCCCACTCCAGCCAG GGCCCTGTATCTGTTTCAGGCC[C/A/G]GAATCGTCACGGCTCACAACTGTGGAGGTAGGAATGACGA G
WI-1936	117 T C	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCTGGTGTGTTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAACCAAGTGGGACACCAAGGGTACTTGTATCACCT[C/CTCCCCGCAACCCCA AGCAGCACAGCTTGACAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGGG

WI-5204	54	C T ...		---	TAGATTTGATTGATGACAATAGGGAAGCCTTTGTTAAATTTGGGTTTGAAGAA[C/T]GAAGAAAA TGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70	A G C T C A A A A A	GGACCTTAAT ATTTAACAGA	AGATAATTTG TAAAGATAGTT TTCGC	TTTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[G]GCGAAAACCTATCTTTACAAAATATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T G A T A T A A	TTGTATCAAA GAGATGGGGT	AATTAAGAA ATCTTTACATG GTTCTTT	CCCTGAATGTGCTTTGCTTCTCCTCCAACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTGA AGAGTACTTTAATTAACCTGTATCAAGAGATGGGTATATAAT/GJAAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTCCACTGCTATCAGTAA
WI-4456	49	C T T A T A G T T C C	AGTTGAATTA TTCAGAAAAT	TTTCTGTTAT GCATGAACCTTG	ACACATTTCAATTTGCTTTAAGTTGAATTAATTCAGAAAAATATAGTTCC[C/T]CAAGTTCATGCATAA CAGGAACACCAGGTTGGGCAATTTGATTGAATGT
WI-4461	49	A G C C T T C C	TCACTGTTATT TTAAAAATTAT	TTTGACCTTTC ACCAATTTCA	CTGAACTAATGAGGTGCTAAATCACTGTTATTTAAAAATATCCTTCC[G/T]GAAAAATTTGGTGA GGTCAAGAAATGAAATCCCACTTTTAGATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75	G A ...		---	CTACTGGATTTTACTTTGCTCAAGCCAGACAAACACGAAAGT[G/T]ATAAGAAAAACAGTTAGTAAT CTTTCACTTTGATTTCTCTTCTACCTCAGGGAATC
WI-4465a	41	A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAAGTGT TCITT	GGGTTAGGACCTCGAGATCTTTCAAGAAAGCAATTCAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCCATAATC[T/C]CTGTGTTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
WI-1949b	160	T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAAA	GGGTTAGGACCTCGAGATCTTTCAAGAAAGCAATTCAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT/GJCAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86	T G A T G C T G A G T	CAGTGGTGAG	CCATGTCAGCA GCCTTG	TGAGAGAGTTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTCTCTTTTATCCTATGATTATTTTTCAGGAAGTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGTCTGCTGGACAAGATGGGCCCTAGGATCATTTT
WI-4529	64	T C A A G A T G	CCAAGTAAGT CTATCATTTCTG	TTCTAAAAATA ACACTTCTGA AAAA	

WI-4540	110	A	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTCCCTTTCTTAAAAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCCTAT TGCTCGGTAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGCATGGCTGCATTGTCCAGTC AAATGAGACAACCTTCCTAT	
WI-4582	226	T	C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAAATTCACCAAAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATCAAGGCCAGTTTAACCTTATTCCTGTACACA AATACTTTATGGGAGACAGCATTTGAATCAATCAATAAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT[C/C]CCTTGCTAGAAACCATTTGAT
WI-1965	105	G	C	AG	GAATGGATGGG TCATCTCTCT	CAAGGGTTAGTTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG[G/C]JAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTGGTTGGTGTATGACAGT CATGG
WI-5248b	99	C	T	TTG	AGAAAAAGAG AAGAAAGGAA AAA	TGTTTAAAAACCATAACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAAAATTAACACGCCTAC CATTTTCACTGTTTTCTATTGACCGTACTTG[C/T]CTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38	G	C	CTACGTTGTT	TTTTAATTTTC TGGGGTTGCT	TGTTTAAAAACCATAACAGTTTGTGCTGCTACGTTGTAA[G/C]JAGCAACCCAGAAAAATTAACAGGCC TACCAATTTTCACTGTTTTCTATTGACCGTACTTGCTCTTTTCTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69	T	A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTTGCTGTAAGCAGAAAGCACTGTGA CT[A]CATATTAGGCCCATCTCTGCTGAAAGCCTGCCTACAGCAATTTGTAAACATATGGCATTTGGG ACATACTCTGAGCCCATCAACTATTTGACAAGATTCTCTTTTAAACAA
WI-5252	119	A	C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAGAAGTCTTGGGAAAAGGATTTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATAGTAAATACCTGTGTGAATCATTTGCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61	A	G	CT	TAGGTGCTTA AGTTGCTACT TGG	TGCAAAAAAGGAAAAATGATAACCCAGGACTGTTGTTCAAGCAATGCTAGAAAAATTTGCOCTA[A/G]C CAAGTAGACAACTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTGTCATTAAAGTCTCTATTCA ATTACCATTTATCGGGTAATTAACACTGGAAGTAATGCCAGGCTAAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77	C	A	GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAAGAGG[C/A]CTTTTCATCTGCCCTCGGTGGGTTTTTCAGTAAGTCAACATGTCTTTGCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCCTACTCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50	C	T	TTCCGAATG	TGTTACTAGGTG TACTTACAAGA AATCATC	TCAGTGTAGAAATTTCTTCTCCTCAGTGAGACCATTCTTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAAATTAACAAAGTACTTGCTACCTGAATTTGTATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A	G	G	CTGAAGTGTTA AACTGGATTG G	GCACAAAGAA AGTATAAGTT G	AACTGTGGTATGTATTGTTGTATTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAGATATCTCAAGACATTTAATCCTAGAAGCACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACTTCAGTAACGTT
WI-4677	82	T	C	AAA	TTTCAACAGTG TCATTATTCAA CTT	TCCAAAAGTG ATTAGGTGAA AAA	AATTCAGATTTTGAACATACGTCGACATTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAT GAGTTGAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGACTAGAACACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTTCACTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTTGGACGGGAAGAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATCTG
WI-4722	88	G	A	AACACCAC	AATATGGAATC TGCAATTCAGTT G	TGCACTATGG AACACCAC	CTTCCCATTTCTGCCAGTTAGATGACTGCCTCTCCACCAGCTAGAAAAAGATGGGAGATTATTTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTACAGAGGAGAGCTTCTGAAGATCAGTGTATTGTCA TAAAGGTGAGTAAATCACTTTGATGGTTGAGATTTTCAAGAAACGTGAAATTTTGAAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACACGAGTGTGTCTAAAAAATATGATAGTTTCTTCTCCTGTCCACC GCAATGAAAAGGAGTT
WI-2028	176	T	C	CCTGCTCATC	GGTTGGAAACT CAAAATTACCTA GAA	TGTTTACGTTG CCTGCTCATC	GACTACAGCGCACAGACAGGCAATTTGTGGCTTGCACAGGTGTTGGTTTGTGTTAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGCTCTTCAGTTTACTACAGACCTCATCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCTCAT[C/T]TCTAGGTAATTTGAGTTTCCAACC TGTCG
WI-2033	183	T	C	A	CAGTGGTTCCA CGTTCTCC	GGGTGCTAGA ACTAATCCCTC	ATGTGTATGAGCTCCACATTGCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTCCAAAGTTATACAGGACCAGTGTGGAAATTT AGCATTTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTTGGAAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAGAGAGATCAACTGGG TAGAATAACTCATCGATCCACCAGGCCTCCTCCACCATTCTCCATCTACTTCTACTCTGA[T/C] AGGCAGACTTATGAAAAAAGGGA
WI-2034	150	T	C	CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACAGTGCA CCAAGGAC	CCACGACTATGCTTCAGAGTCCCTGGTACTGACAGAGAGGCTTTGAGGACCATTGTGGCGCCCAAGA CCTCCTCTCGGGTTTCAAGTGAAGAACGATGAACCTCCTTCTATCTCTACAGAGCTGAGACTTCAACA CAGTGCACCAAGGAC[T/C]GGACCTGCACCTATCTTTTACCCCTCCGACACCAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTGCTTTAAA GTGTGTAAGT ATTAATTAG	ATTTCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACCATTGTCTGTGTTATTGTCTCTTGCAAGTGT ATCCAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAAAACTGTGCTTTTAAAGTGTGTAAGTATTA ATTAGATTTCTATTTTGTATGATC/TTTCAAGAGGAAAAATTTGTGTAAGAGGATTCCCAAT TGCATTTCCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTTCTG GTTATTTTCT GTTG	TCATTGACTTTTTAGAGTTCTTCCAGTCTTATGTCTTATTTTCTTTAGGAAAAAACTAGGCTAGGAGAA CACAATTCCAGGTTCTCTCCAGATGCAGAAGATACTAGAAAAATGC/TTGAAACAGAAAAATAACCA GAAGAGTTCAATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAAATCATCTTGTCTAAGTTCC/AG TTGAAAAAAAATATGCCAAAAATTTTAAATTTTATCCAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTTAAAAAGATGGCGTATCACCTCA
WI-5300	38	T C	TCCAGAGAC CACTTCATTC	CTACTCTTTCT ATTTTATAATC CAAAAA	CTTACTTCCAAAGTGTTTTCCAGAGACCCTTCATTCT/CTTTTGGATTATGAAATAGAAAAGAGT AGGTGTTATTATCTCTCTTTTACCAAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTGAGTGCAGAGGCCA
WI-4818b	121	G T	TGATAATGGG GCCCTGTT	CCTTCTCTTTA TATGTATGCCA GA	TATAATGTTTTGTTCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAAATTTATTCAGAAGGAAAAATATACATATGGGTGATAATGGGCCCTGT/TTGTTCTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C	TTGCCATAGAC TAGGTTATGTC	CATATGTATAT TTTCTCTCTG ATAAAAT	TATAATGTTTTGTTCATAGTTGCCATAGACTAGGTTATGTCC/AG/CACATGAATAAACAATCTTAT ATAAATTTATTCAGAAGGAAAAATATACATATGGGTGATAATGGGCCCTGT/TTGTTCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	TTCCATTTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTTGTGATCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATACAAATTTCAACTCAACAGGAATCCATTTCTGGTAGCAGGT ATAT/CTGGACTCAATTTCTCTTTGCACTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATTCCACTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA/G/ATGAAT AAATGAGTAGTGGAAATGCTTGATAACTGGAGTAGTGCCTT
WI-5328	44	A G ---		---	AACATTTTAAACCATGCTACATTTTACAAACACTGAAAAGACAG/G/AAAAAAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAAAAT AGAAACACGTTGATACTGGAAGGAG
WI-4897	93	A G ---		---	GCCTTTTGTAGTTAAGTCTTTTGTGAGTGTGCTTTTTTTTCCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAGAAAAAATAGCGCTTGG/G/AGATAAACACATCTTC
WI-5345	29	G A ---		---	CCCTGCTATAGGTCAGTTTAAAAATCCT/G/AG/CCTGCTATGGTTGCTTGTGTAAGGCCACATCCACT GAGGTATATTCTGTCTGCATTTTCTATATCACTCAGCTTCAGATCCCACTCCATCAACTTGCAG

WI-5370	143	T C	AATAAGATGG TACCTTAACCTA	CAAAGTTGGTA CAGAGAAATTC AAA	TGCATGTTACTCTTGGAAATCATAAAGGGATCTGAGAGCCTACAGTATATGGCAACATTAAACCAAT CTTTTGAATAATTTACCTGTATCCCATCATGGTTCATTTGCAAAAAAATAAGATGGTACCTTAACCTA ATAAACAAATTCCTTGAATAATCTCTGTACCAACCTTGCTTTTC
WI-9711b	423	T A	---	---	GATCCTTCATCCCTCTCCAGAAGAGGAGAAAGGAAACACAAAGAAGAAACGCCTGGTGACAGAGCC CCAAATTCCTACTTCATGGATGTGAATGCCAGGTGAGGAGACGGCTTGCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTTAGCTGCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTTCGCCCTGTGGAAATATTTCCCTGATACTCTTAAATTTGAATG
WI-9711a	390	C A	---	---	GATCCTTCATCCCTCTCCAGAAGAGGAGAAAGGAAACACAAAGAAGAAACGCCTGGTGACAGAGCC CCAAATTCCTACTTCATGGATGTGAATGCCAGGTGAGGAGACGGCTTGCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTGTAGTTAGCTGCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTTCGCCCTGTGGAAATATTTCCCTGATACTCTTAAATTTGAATG
WI-9702c	345	G A	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGTCTGCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCATTCAGCAATCCCTACTGGTATGTATCAGGAT AGAGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATTTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATTCCAGTGTGCTACAGCATCTGATAG
WI-9702b	344	C T	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGTCTGCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCATTCAGCAATCCCTACTGGTATGTATCAGGAT AGAGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATTTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATTCCAGTGTGCTACAGCATCTGATAG
WI-9702a	179	C T	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCCGTCTGCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCATTCAGCAATCCCTACTGGTATGTATCAGGAT AGAGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATTTCTAACTTTAATGATCTCTGTG CTTTTATACTAGCTTTAAGAGGTTTTCATTCCAGTGTGCTACAGCATCTG
TIGR- A003N21	49	C A	---	---	TATAGTATTTAACGAAGCCTAGAAGCAGCGCTGTGGGTGGTGAATTTGGTTC/AJAGCATATCTTAGGT ATATAATAACTTTGAAGCCATAACTTTTAACCTGGAGTGGTTGATTTCTTTTTTAATTTTATTTGGGA GGGTTTGGATTTTAACITTTTTTAAATGTTTAAATATTAAGTTTGTAAAAGTAAAGGAAACCATCTCTG TGATTACCTCTCAATCTATTGTT
TIGR- A004V30	203	C T	---	---	AGAATGGCTACTTCATAGGGCAGAGCAGCCACTTTTGGCTAAATTTTAAACATCCAAAGCTAAATAAT AATCAAGAAGAAATAGAGAACATTAAACAAAATAAATTTATGTTCTATTTGGGAATACCTAATATCAG ATACTAACAAGTACAGTGATAAGAAATAAAAAAGATAATAATACACATACCTTCTAGGTTAGTAGA AAAGC/G, JCTTCTAGGTTAGTAGAAAAGTT

[illegible]

WI-7593	46 G A ---	---	TTTGTGCTGACACCCACTGCTCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTTTGGG CACTTCCTCTTGAAATATAAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCCAA
WI-6962	78 A G ---	---	AGTGCATCTGGGGAAGGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTT GATCCAGAG[A/G]GACAAAGCTCCTCAGTGAGTGGTGTTAATCCAAAGACAGAACCCCAAGTCTCC TGACTCCTGGCTTCTATGCCCTCTATCCTATCATAGATAACATTCTCCACAGCCTCACTTCATTCCAC CTATTCTGAAATATTCCCTGAGAGAGAACAGAGATTAGATAAGA
WI-7059	43 C G GGCATC	AAGGACCCCA GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAGGACCCAGCCATC[G/G]TGACCCAGCGGAGGAGCCAA CTATCCCAAATATACCTGGGTGAAATATACCAAATTTCTGCATCTCCAGAGGAAAAATAGAAAAATAAA GATGAATTGTTGCAACTCTTAAAAAAA
WI-9063	53 A C TT	CACTTCACTGA AAGACACCAT	AGCAGCCATCACATGATCTGTTTTTACCACCTTCACTGAAAGACACCAATTTAT[AC]TACCCCAAGGG CAGAAAGTAGAATCTACTATTCAATAATGTTGACACAATTGGAATTGTC
WI-7079	293 T G ---	---	AAGGGCATTGAGACTATAAGCAGTAGACAATCCCAACATACCATCTGTAGAGTTGGAACGCAAT CTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTTATTTCTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTAATACATTTATACATCACTTTTGTGACTTTTCCAAAGCCC TTTACAGCTCTGGCACTTTCTCGCTAGGCCTGTGAGGTAACCTGGAT
WI-9074	38 A G AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAAGTTCTTTTGCTCTAAAGAA[A/G]AAGGAACTAGGTCAAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAAGATGTTGCCACTGGCAAATGTAACGTG
WI-7104b	249 C T ---	---	GGAGTTGCCCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCACAGAAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCAGCATCTTG[C/T]
WI-7104	157 C A ---	---	GGAGTTGCCCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTGAGGCCCTTGACCCAGGTGGGGCCACAGCACAGCAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T CTTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCCAACCTCATTTTAGTTGCCTAAGCATTGCCCTGG[C/T]TTC CTGTCTAGTCTCTCCTGTAGCCAAAGAAATGAACATTCCA
WI-9014c	93 T C ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCCAGTCATCTTCTCTCCAGAGAGGTGGGGCTGGAT GTCTCCATCTCTGCTCAACTTTAT[T/C]GTGCACTGAGCTGCAACTCT

WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCCCTCCCCAGTCATCTTTTC/TTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTCCOC TCTTTTGGCCCCAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTTCAACAC A/C/A/CACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/C/CCCTGCGT GCTCAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTG CCCTCTTTTGGCCCCAGTATTCATGGCAGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTTCAA CACACACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCTGCTGGATCCGGGACCCCTTTGCCCTTCCCTC/TTGGCTCCAGCC CTACAGACTTGTGCTGACCTCAGGCCAGTGTGCCGACCTCTCTGGCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAGTTGTGGAAGCAGAGAGAAAGCTGGAGGAGGCCGTGGGCCAAT GGGAGAGCTCTGTATTATTATTAATTGTTGCCGCTGTTGTGTTGTTA
WI-9171	62 G A ---	---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAAGAAAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAGCTTGATTCAACAGACTTCATGC
WI-9174	47 T C T	CTAGGACCC ATTCTCTATT ACTG	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTATTC/CJ/CAGTCTCTGTCTATATA CCCTCTAGAAACAGAAAGCAATTTTATAGCAGCTATGGTCAAAATGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA	CAGAGGTCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAGAACAGAT/GJATCCCTGTATT TCAAGACCTGTGTGCACTTATTTATGAACCTGCCCTGCTCCACAGACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A	CCACTTCTCCC CGCA	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAAAACAAAAATGGCATCACCTGTCAAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]/ACCTAGGTGAGACTTCCCTTTTCATCTT
WI-9193	94 G A	AGAAATATTGT CTGCCCTTAAAG CA	GGTGTGTGTGG TAGGGGG	TTGGACAAACCTAGAAATTTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGATAA CTCAGAAATATTGTCTGCCCTTAAAGCA[G/A]/TACCCCTCCCTACACACACACCCCTGTCCCTC
WI-9015	48 C T ---	---	---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATTTGGGCTGGATTG/C/TTGTTGGTTAATACAT CTTTCCCTAAAGAAGATAAACACAAATCCATTCAGGTAGTCTGGCACCACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGGAGGTCTGAGAGAGGAGGACAC/A/GTGCTCCCTAATGACACCCACTCCTAGCC CTGAGGCTCGTCCCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGAGCAGCCACTCCTCAATGC TCAATGGCTCCCCCTGAAATCAAGACAGG

WI-9231	32 GC	CAGTCCCA GATTGA	CATTGCCAC ACTCAGAC	GTGACCTGTGAGGTCCAGGTTGAGTCTGAGTGGCAAGTGTGTCAAAAGGGG TGCCCCCAGGAGATAGGCTGAGAGCAGGAGTTGAGCCGGAAGAGTCA
WI-7836	120 TC	CAATAAACA ATGCAACGTT C	GCTCTCAGA CAAGATTAGA AATC	TTGTTTGGGAAATAGAGTTGAGATAAAGTCTCTCATTGAGTAGTTACTGAAAGAAACTCTGCTA GAATGATAAATGTGATGGTGTCTATAACTCCAAATAAACAATGCAACGTTCC[T/C]GATTCTTAAT CTTGTTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACAGCT
WI-7286	65 TC	CAGTTACGCT TAAGTGACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCCTTTGGCCCTGCAGCATGTGATGCTCCAGAAATTCAGCTTCAGCTTAAGTGACAGAT/C TGTTAAAGCTTTCTGTTAGATTGTTTTCAGTTGGTGATCATGTCTTTCCATGTTGATCTGTAATATT TTTCCATCATATCTCAAGTAAAGTCA
WI-7858	91 TG	CTAAGCATGT ACGTGAATTT TAAAT	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAAATCTTGAAATATCTCAAATGTTAATAACAATGAAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAATTTGTTATAGATGTAAACTTTTAAATAAATTTGGGTGTGG
WI-7860	50 CG	CGTACCTCAA ACATAATTGA TTC	---	GAAATTAAGGGAGGTGTCTGTGGTCTCTCCCTGCCCTCTCCCA/C/A.GTGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCTGGACCTGACCTACTGGGCTTATGGTTGGGGTGTAGGCAGG TGAGCGTAAGTGGGAGGGAATGGTAAGAAAGTCTACTCCAAACCTAGGTCTCTATGTGACAGCCAG ACCTAGGTGCTCTCTAGAGGGAACAGGGAGACCTGGGGTCTGTGGAT
WI-9064	29 AG	CGTACCTCAA ACATAATTGA TTC	GCTTGAGTGA AGTCTGCAGA	CAAGCGTACCTCCAAACATAATTGATT[C/A]GTTATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGAGGGCTGGCTACTGCTCTCTGCACTCTGCTGCTTG
WI-7307	128 GT	---	---	CACACTGTCTGTTCTTTCAGTGTGGAGGTCTGGCAGGGTCAGGTGGGTAAAGCCGGGTCCACA GGCCCGAGCCCTGGCAGGGTCTGGCCCGCAGGTAGGGAGAGCAGTCCCTCCCTCAG[G/T]AACT GGAGAGGGGACTCCAGGAATGGGGAATGTGACACCAACCATCTGAAAGCCAGCTTGACACCTCCAGT TTGCACAGGGATTGTCTGGGGCTGAGGGCCCTGTCCACCCCGCC
WI-9274	25 CT	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACCTTTGGTG[C/T]CAATGGACAGAAATTTACCTGTGCTACATAGGAGAA GTTTGAATGCACCTTAATAGCTGGTTTTCACCTTGATTTCGAGGTGGAAA
WI-7313e	266 TC	---	---	AATTCCTTTCTGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAAT TGTTTGCAGCTTTTATGTTTATTCATAGGTATAGGTGACCTAAATCCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTGTGTTTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTGTAACTGAATAGAATTGTATAGCGATGA
WI-7313c	256 CT	---	---	AATTCCTTTCTGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAAT TGTTTGCAGCTTTTATGTTTATTCATAGGTATAGGTGACCTAAATCCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTGTGTTTATGTTTAAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTGTAACTGAATAGAATTGTATAGCGATGA

WI-9281	68 G A ---	GCTAACACTTT TTAAACCCTG CTC	--- CATTTATTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/A]TGTAGTTTGCAGTCTGTGTGCTTCCCTCTCTTATGACTGTGCC
WI-7848	142 A G CTC	GTATATTACA ATGATCACCG ACTGA	CCCACAGAAC TATTGTAAAC AA	TTCTGAAATATAACCAGCCATTGAGCTATTTAAAACTTGTAATTTTTTAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCGCGTGACATAAAACATTAATGCTAACACTTTTTTAA ACCGTCTC[A/G]TGTCTGAATAGCTTTCAAATAAATGTGAAATGGT
WI-9304	70 G A ACTGA			TCACGTTTGGTGCTTCTCAGATTTCTGAGGAAATGCTTTGTAATGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTTACAATAGTTCTGTGGGCTGTTTTTTTGT
WI-7933b	314 C A ---		---	TTACAGAACTTGCCTGTGCCTGTGCTGCCCATGCTAGGGGGGAGGGGCTTTTCCCTCTCTTTCC TACCTACCCCTTTTCTCTTGGCCAGGGCTCGATCTACCTTCTCTGTCCTCCCTGGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAGAGCTGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCCTGGGGAGGAACCATAGCTCCCT
WI-7933	96 G C ---		---	TTACAGAACTTGCCTGTGCCTGTGCTGCCCATGCTAGGGGGGAGGGGCTTTTCCCTCTCTTTCC TACCTACCCCTTTTCTCTTGGCCAGGG[G/C]CCTGTATCTACCTTCTCTGTCCTCCCTGGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGCCCTCGATGCCAAATTAGCATTTAGTATTTTGC CAAAGTCTAAGGGACCATGGCTGCCTGCCCTGGGGAGGAACCATAGCT
WI-7374	182 T A ---		---	CCAGATGTGCCCATCACGTTTTTTCTGAGGCTTTTGTAATTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTTGACTTTGTTAAATATTTGAAATGTAAATGAAAAGAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTGAAGAATATATTG[T/A]CAGAAACACAAAGGCTT GAT
WI-9343	78 C T CCTCTGCCA	CCAACAACAT CCTCTGCCA	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCTGCTACCTTGACCTTCCCTTCCCTGCTCTCTCTCATCATCATTCCTCCCAACACAT CCTCTGCCA[C/T]ACACAACAAAACGTAAGTTTCATTTGGGCAA
WI-7386b	104 T A ---		---	CTATATGTGAGAGGCGTGATCTCGATGGAAGTTGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAACAAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75 A G ---		---	AAGAAGGAGCTCAGTTACGGGGTTTTAAACCTTCATGAAAACCTGAAGAGTTACACTTTTGTATTAT GCTCTT[A/G]TGATTTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79 T C TTGG	CTTTAGAAAA TCTGCTTTAAC TTGG	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAACTG CTTTAACTTGG[T/C]ATTCCTCTAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107 T C GTTCC	TGCTGGGCTGT	GGTCCAGAAGA GCGG	TGCTCCTGTCCCATCTGCAGTGGACCCCGCCCTTTGAGGAGGTGGGGTGAAGTGCCTCTT GGCAGGATTTGTGACACTGCATGCTGGGCTGTGTCQ[T/C]CGGGCTCTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTTGGTCTGGGAGGTGGTGAAATAAAGGCATACTGTCT

WI-7424	131 T	CAAGAGAGAG AGAGGAAAGA A AAA	TGCAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGGGAGGGGAAGAGCAGAAAGTTAGAGAAAAAGCCACCGGAGGAAAGG AAAAACATCGGCCAACCTAGAAAAGTTTTTCATTCGTCAATCCAGAGAGAGAGAGGAAAGAAAA T/AJACAACTTTCATCTCTTCTTGCAGCTTCAATAACATCTACATA
X86400	118 A C		---	TCCTGCAAGAAGTTCTCAAGCCTTTTGATTTTTGTGCAATAAAGTACAGCTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTCTCTCTAAATTTAAGTGAGA/A/CJTCTTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAATCTAAAAATTATGTACCACCTGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTCA
WI-8053	242 T A		---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAAAGTGTCCTTAAAGGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAGGGTCACA ATTAATTCITTTGATCTTTTTACTCACTGTTAACTTATATAAT/AJITCAGAAC
WI-6190	165 G A		---	TACACAAATGAATGCTTTTATTTCGGTATGCATCCACATTTTCAAGCATTTAGTGGTCTGAAACAGCAAG TGGAAAGACGCAGCAATTTGCCAGGAGGTCAAGCCCACTTTCGGGATCTGCTGTGCACACCGG GTTCTCTTAATCCCTGCTGAGGATCTTG[G/A]GAAGCAGCAGCAGCAACCAAAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTACAGATTCCTCAAACTAGACCCCA
WI-6275	148 G C		---	AACAGTACACCAACACATGACAACTCGCCAGGAGGCTTGTCCCTCCCTCTTGGCTCC ATGTCCCTAGTCAGCAAGGTGGGGAGGCAACCGATGTTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAAAG/G/CJGGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTCAGTAACTGGTATGCTGAA
WI-6421	41 G T		---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGT[G/T]GGGCTTCCTGAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACA GAATATTTGGGGCAGAAACCTTGAACCTGGCCACCGGACATCCCAATATCCCTCTCTCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T A		---	GGGTGAGACGGGTTATTGTGCACATTTACACAGCTCACAGGCTGGGCTGGCAGCGGCTGCTC CTGTGGTCGGGCTGCTCTACAAGGGCTTCACTTTTCTTCCACACACTATGTACAGTCAGTCTCCAA GGTGATGGGCTACAGTGTGCTGATCAGTGTGATGCTGTACACACATTTTACATAAATTACACAGCTC ATACATGAAAAAT/AJAGAGCCTAAGGGCTGTATTTTAAATGAGAAAAAA
WI-9420	202 G A		---	AACTGTTTACAAAAATAGGCTTTGCAAACTTCATTACTGAATGTAAAGTCAATGACTGTGTTGTTT TAAAATATGTACCAAGGAAATACAAATGGATAATGATCATTTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCACAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCATTCTTCTCACCTTAACTGCAGCTGTGCAAGATGCCCTCAGTGTG

WI-9448	184	G A ---	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGAGCACCTAGTAGAGGAATACCTGGGAGAGAGAC TGCCCTGGCCATGGTGGTTAAACCTACATAGAGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTTAAGAAAAATGGGCTTGTGGTTCCAAGGCTGAGAGCTGGACCAAG[G/A]CACTGGTTCTTAA TCTCTGGCTTGGATTTATCCAAAGGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A ---	---	ATGTCAGAAGAGACACAGACAGAGGATTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGGAATATGATCTCCCTAAAGCCCCAGATTCCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTCCTGATGCAGATCTGCTGTAGCCATGTCTGGCATCACAGGGTGGT TTATTAATTTCAATTCATCTCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTT[G/C]GCTGATGCAGATCTGCTGTAGCCATGTCTGGCATCACAGGGT GGTTTATTAATTTCAATTCATCTCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TTCAGTGATAAGGACAGGTCTAGAACAAAGCGTTCCCAACCCCTGGCACCATGACAGTTTGGACCAAA TAACTCTTTGTTTCAGGGACTGTCTACACATTGTGGGATGTTTAGAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCAACAATCATGACAATGAAAATGTCTTTAGACATT GCCAAATATACCTTGTGGACAAAATGGCCCTGATTGAGAACCCTGTT
WI-5385	110	G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTAACATATGTTTTCTTGGCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGAACAATTGAATGCA
WI-5403	199	T G ---	---	ACCAAAACCGTTGGCAAAGGCTCCCCAAGACTCACCACCCCAACTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCAATAATAATTTGCTACAATTTTCCAGTAGTTACCAGGCACCAAGCCTAT TGGAAAGAAATCATAAATGTAAACCTACAATGTATTGCTCTCTGGCTTGGTGCCAGGCATAGAGTT[G/ JGGCTACAACCCATTTTATCATTTGAACCCCTCAGAAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---	---	TGGTATTTTCTCTTTCCTAAAATGTTATGATTAATTAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGAA[G/A]AGGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTCCCTTTCCCTAAATGTTATGATTAAATAGTGTCTTTG[A/G]GAAATTTGAAAAATGT AAATCAGAGAAACAGAGAAAGAAAATAAAGTATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCC TAGGAAAGAAAGAGAGCCTGGGAAGAGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5696	61 C A ---	---	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCAATTCAGTCTGCATGAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCACACCGAGGACAATGTTGAGAACTAAATGACTGCAGGTGAGCAATTCCTGTATT TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGGGTGAGTTATTTTAACTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGAGCTGTCTC[CT/TT]GTTCCCTGTTGGTCCCCGGAACCCAGTGTGGTGGCTGGCACAGAG GAGGCCCTGAGTAGCATGTCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTGGTATACCTTCTCTTCTGAAGACCAACCTTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTCAGATGTACTTCTTACATCTCTGAAAACCTAGATGAGTAGGCTCTCTTCATCT CAATTGAAAATCTAGAA[G/A]AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTTGTGAAGCCACACAGAAAGTGTACTCTCTTAC[C/TT]AAGTGTACTTTGCA TATATTTATGGGATGATTCTATCCCTACTTAAGATTTCTCTCAGGTTAAATATCCATTTCT TTGTTCAAGGAGTTCTTATTGGCCTTCTTCTAAACCTTAACCATTCCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAACCTCGTTGGCTCAAAGGAAACTGTAG[A/C]JAAATCTTTTTTTTTTTTATTTTTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTGTGATGGCACGCTGCTCTTTGTTTGGTGTAATCCTCTAGT GGCACCTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAAGCAGACAAAACACTCCAAGAATAC[A/G]AGATATAAAACATCATCA GTAGAGATGGGATGACCTAGGAGGTCACTGCTGATGAGGCGATGCAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTTGCCCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAACTGAGGTAGAGTACAGAGAAAGAAATTTCA
WI-11152	179 C T ---	---	GATTCCTTGGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGTCTCGCACCAGGGGACTGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAGTGGGACAAAAGGCTTGTC[A/C/TT]CTGTCAGAAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167	A	G	---	---	TGGTGAGGAGCTGTAAAGCTGAAGCTGCTCTGGCTCTTCGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCTCTTCCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACTTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGT/GJTGAACTTGAGCAAGTGCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198	G	A	---	---	GGGTTCAATTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACAACACATTAAACTCTCCTCCCACTCTA CCCGCCAAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164	C	A	---	---	TTATCTTTCCAAACCATGTGTGTTTCTTCACATACTTTACGTAATTTTAAATCATGTCTTTAAATTA TGCACCTACTTGTGGCTACCAAGACATGCTTCCAAATTGTAATCCCTAACACAGCAAGCATAAAT GATGTGCCATCTTTGTAATCTCTAAAG[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACTCTCTGTAATTTCCCTATTTCAGCATTCATGATTA
WI-4860	72	A	G	---	---	AAAAAACAACTTCATTTGACATTTCTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTTGCCT GATTT/GJGGAGATAAACCTGATCTCTAAGAAAAATTAACCAAAAGCAGTACACTAAAA TAGCCT TTGTGTGTGTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAAATAATGTTTCATATCA CTCTAACTCCACATAGAGCATTAATATAGCA
WI-9705	111	C	A	---	---	TGAAAGGACCAGTTCGAATGCCTACCAAGTAAAGTAATCGAGGGGCGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCCGCTGCC[C/A]AAAAATTTTAAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGTAGATTGCGGTTCTAGTAAGTAGCTAATGTTTAGATA TGATTTGTTGAATTAATGTTGCTGTTCTTGGTG
TIGR- A004Z48	177	A	G	---	---	CAAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTCATGTAAAGGTGGGCGAGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGGTGAGGGGAGAGATCGTGGGTTCATGAGATCCCAT CTTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAG/A/GTCTCCCAATTCAGGGGCTCCC GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGCCACCTAGAGATG
U17579	34	T	G	---	---	GGGATTCATGTGTCTGTCTCATCCATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTCTTCCC TATGTTCCAGAGACAGAATAGACCTGGCCCCCTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAAGCATGAGTCTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCTTCTAGTTGA
WI-7747b	88	T	G	---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTTCTGTTTGTGTTGGGTATCCTGCCAGTGTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTAAATAAGTATATAATTTTTTATGTTTTGTTCTGA

WI-7747a	44	T C ---	---	GTGAGAGGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCT/CJTCTGTTAACTGTGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTTTGTTGTTGTTGGTATCCTGCCAGTGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTGAATAAAGTATATAATTTTTATGTTTGTGTTCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCTCTTCAGCTCATTTTGTCTCTCACAAATTAAGGGAGTAGGTTAAGTGAAGGT CACATACCATTATTTCCCTTCAACAAATAATAATTTTACAGAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGTTATTTTATATTAAAGCCTACAACATTTTTT/CJAG TTTGCAATAGAACTAATACTGGTGAAAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---	---	AGCCCCAGCTGGACTCATGGATGTGCACCCCTTGTCCCTGCTCTTCTGCCCTGGG/AJCTCATGTA TCTGGCAGCTCTGGTACCCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTGCCCTGAAGCT GAGAAAGCACAGGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTCTCTTCATCCCATCACCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG G/G/CJAGAAGTGAAGGAAGATAGGAAGATATACCTCTCTGTTATTTTTTAAAGAAACATTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTAGAGGCCCTAATTTTATCTATAAATATATTAATAA AGCAAGTCAAACTTGGATGATCAAGGTAAATTAATGTCAAAAGTTTAAAT
WI-7919	242	T C ---	---	GAAGGCAGCTGGATCACTTCCCGCAGTCTTGGGCAGCGCTTGTGTGGAACACGAGAGCTCCTCCT CAGGGCCCTGGCACTCACTTCTATCTGTATGATGATGTTGGTTAAACACTGTCAAAATAATAGAGAT GTGCCAGATTTAGATTTTCTTACCCTAATCTGTGTTAATATTGTAACCTTTATCCATTGAAAGTGCA AGCCCAATTCAGATAAGCTATAATCTGGTCTTTAAGGAAJ/CJACAACTTT
WI-7928	101	T G ---	---	CTCCCTTCTATGTCTCAGCAGCACGTTGGGGCACACTTGTTCATCTTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAACCTGAAATTCACCTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCAATTAATAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAGACTTAAGGGCCCAATGAATTAATATATACATACTGCATCTTGTGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAACJ/A ACTGAATGAAGAAATTTTGGTAACAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACAGTTTCCAGCCCGTTGCCCACTCATCTCGCGCTTGTGTTGGTGGGGGCAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCATG/CJAGCCCAAAGTACAGCCTGGACCCCTGGTGTG TGTAGCTAGTAAGATTACCCCTGAGCTGCAGCTGAGCCTGAGCCCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGGCAATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---			TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAATATTTTATACACTCTTGTGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGT/GTGTAAAGGATCTCCACAATGCTGCAAGTGTG AAGCAGGTTTCATTTGTGAATAGTTTAAACAGTCAGGAAGGCTAACTGGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCATCTGTGTTACTTACTTGGCCCTTTTATCTTCCCTCTGGCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGCCTTGGCAGTGCT [G]TCTACTCCTCAGGTGCAGCATACATAACCCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAAATGTCATCAG
WI-140	252 C T ---			ATTTGAAGATTGGAGGGCTTTGCAGAGGAAAATAGATTTCAATTTGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCATTGAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTTAGTTTAAAAATGTGTCATTTGTCTGTATTGGCATTCCT[C] GAGGCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTTCGCCGGATCAAGTCTGGCACC CATGATGGAACCTTGGCATGGTTTGTAGTACCCTGGACCAAGTAGTCACTCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCCACTTCCCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC[C]TGTTTAAACAAGCATAGATAATTTCTGAACAAC
WI-198	218 C T ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAAGAAAATAAGCCTCATCTCTAACTATGACTTGGTCGG AAGCCAAGAACCCTACTTCAACATTTGACCCATAACCTTCTCTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG[C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCCTTATTTTGTGTTAGTCCC
WI-205c	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAAGAAAATAAGCCTCATCTCTAACTATGACTTGGTCGG AAGCCAAGAACCCTACTTCAACATTTGACCCATAACCTTCTCTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG[C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCCTTATTTTGTGTTAGTCCC
WI-205b	146 T C ---			GAAGACTGAGTTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGAACCCCAAGTNCCTTCAAGAGGTCTCAGACTACCTCCATCCCTCCCT CTCCCCACACACAAAATACAGAGATTG/CJAATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTGTGTTTCTCAAAATGGGAAATGG
WI-234	165 G C ---			AGCTTTTGAAATCCAAAACCCACATTA/GCTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACCCCTGTGGCTGCTGAAAGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-276b	25 A G ---			

WI-276	25 A G ---	---	AGCTTTGAAATCCAAAACACATTA/GCTTGACTCTCTTATCCTCCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACCCCTGTGGCTGCTGACGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGCAAGGGCTTTGCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	TTTCCCAATCCACAGGTAACATAATAATGGATGTAGAAATTTAGAACTACTTCC(GA)GTTT TTCCCTGGGAAAATATTCACAAAACATTTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGCCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAATTATTAGAGCCAGGCTTGCTCTGTGACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA(T/C)AAATGGTCTTTTATTTAAAAAAA AAAGNTATCTAAAGAGAAAACCAATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCACTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA(T/C)AAATGGTCTTTTATTTAAAAAAA AAAGNTATCTAAAGAGAAAACCAATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCACTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAA(T/C)AAATGGTCTTTTATTTAAAAAAA AAAGNTATCTAAAGAGAAAACCAATAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCACTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG(A/G)TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAA TTGATCTAATATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG(A/G)TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAA TTGATCTAATATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGCTATGTTGAAGAAGTATCCTTAGGATATTCT GAT(A/G)CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAA TTGATCTAATATTCTTCACTAATAATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---	---	---	TTCAAAATTTAACACCAATTGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCCTTCTATTGTCTTGACGTATTAACTGATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCATTTCTGCTGACCCCTCCCTCCCTCACCCCTACTTGGGCTCTGACTTCCCTTCTCTGGGCT GAACCTTCTCTGTGTGGCTGTCCGCCCTTCCCTGCTGGGCTCCCAATAC
WI-681b	156 A G ---	---	---	TGAAGCCCTCTCTCTATACCAAGTGTCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCAGCTTTGNCCTGGTATGTCATAAGCAA TCCATAAATTGTTATAGCTATTJ/GJTTATACCTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAATCTGTGATGGTTT
WI-681	156 A G ---	---	---	TGAAGCCCTCTCTATACCAAGTGTCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCAGCTTTGNCCTGGTATGTCATAAGCAA TCCATAAATTGTTATAGCTATTJ/GJTTATACCTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCTTTAAGATATGCAGCAAGCACAATCTGTGATGGTTT
WI-867b	119 G A ---	---	---	AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCAGATCTTCCCTTTTTCATCTCCG/AJTTGTGTTTGGC CAAAATAATATCTCCCCAGGGAGCTCTCTTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAACAAAGCACACATTAGAAACTTA
WI-867	113 A G ---	---	---	AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCAGATCTTCCCTTTTTCATCTCCG/AJTTGTGTTTGGC CAAAATAATATCTCCCCAGGGAGCTCTCTTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAACAAAGCACACATTAGAAACTTA
WI-867	119 G A ---	---	---	AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCAGATCTTCCCTTTTTCATCTCCG/AJTTGTGTTTGGC CAAAATAATATCTCCCCAGGGAGCTCTCTTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAACAAAGCACACATTAGAAACTTA
WI-871b	123 C G ---	---	---	TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCACAATGTAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCAGCCACCTACCTCATG/C/GJAACCTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCACGTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTTGTACATAA
WI-871	123 C G ---	---	---	TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCACAATGTAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCAGCCACCTACCTCATG/C/GJAACCTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCACGTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTTGTACATAA

WI-884	198	T C	---	---	AGGTTCTGGACCTGATGCTGGGAAACAATTTGGGTTCTGGAGAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGAACTTCTCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAAGGAATA[T/C]G ATCCCGCATGCAACATTTATTCAGTGAACACATGATGAAATGAACATAAT
WI-921b	205	G A	---	---	CAC TTC CCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGTGGCACACAGGACAGTTTACTGG CAGTGATGCTCTCACGCTGCCCCCAAGAAAGTCTTGCCAGGAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTAATCAGGAGGAAGAAATCTTCCGAG
WI-921	205	G A	---	---	CAC TTC CCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGTGGCACACAGGACAGTTTACTGG CAGTGATGCTCTCACGCTGCCCCCAAGAAAGTCTTGCCAGGAAAGCAGCATCCATCTAC TCT[G/A]GGGAGAGATCTGACAAATTAATCAGGAGGAAGAAATCTTCCGAG
WI-945c	90	G C	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTTACTGGAGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGTGCAGCACANNNGGTT TTCTCTGGTCATAGAACTCTTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90	G C	---	---	GGCTGGGATGAGAGGTCTACTTGTTGTTACTGGAGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAAGTTCAAACANTAGTGCAGCACANNNGGTT TTCTCTGGTCATAGAACTCTTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167	C T	---	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTTCATTGAGCAACCTAAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTCCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A	---	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTTCATTGAGCAACCTAAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTCCTACC CTGAGGAATTTATCAAAGAT[G/A]TTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C	---	---	TCCCAGTATGGCTTTCAGTAGTTTATTATGATGCGCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATGCTCTGACCCCTTCTGTTGTTG CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATTGCTGCGCTTCAATTTTGTAATNTG

WI-1147b	204	G A ---	---	---	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGCCAGGGTTTACAGGATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACGCAACTTCTCCTCCCTGCTGGCTC CTGAGCCAAAACACAGGCATTTACCAATAAATCACCTTTGTAGATGAACCTATCTGGCCAAACTGATA CIG/ATGCAATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147	C T ---	---	---	GCATTAGAGGGTTCGTTAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GJGCCAGGT TAAGTCTGGGG/C/TTCTGGGGTCAGGCTGCCTGGGTGCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G ---	---	---	GCATTAGAGGGTTCGTTAATGACATTCAGTGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GJGCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTGCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C ---	---	---	AAGTTTACAGAAAAAATACCAGAAAAGTGAOCTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACAGACACTTATCCCCTAGACAGCCATTTCTTTTGAATGNT/CJGNCANT AAAAATGATTTGAAATTGGGAATAAAGCCCTCCCTCTAATGATTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202	C T ---	---	---	TTCTCAATTCCTCAATCTGTGTTACTTTTATTTCTTTCTTCCATCTATGTTGGTAAATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C T ---	---	---	TTCTCAATTCCTCAATCTGTGTTACTTTTATTTCTTTCTTCCATTC/TATGTTGGTAAATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T C ---	---	---	TTCTCAATTCCTCAATCTGTGTTACTTTTATTTCTTTCTTCCATTC/TATGTTGGTAAATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAAT/CJTNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C T ---	---	---	TTCTCAATTCCTCAATCTGTGTTACTTTTATTTCTTTCTTCCATTC/TATGTTGGTAAATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNNATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G ---			TTTCTGCAATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCGCTGGGTCAATTTAGAGCCATAGAGATGAAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCC[T/A/G]GC
WI-1306	240 A G ---			TTTCTGCAATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNTNG GGCTGGGTGACTGTGCGCTGGGTCAATTTAGAGCCATAGAGATGAAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTT[A/G]TCTCCTAGC
WI-1307b	118 T C ---			GACAAAGGTGGTACTAGTTCCAAATCCAAATCTATGTACACTTCTCCTCCTCAAGTGGACA GATTTCTGCATTATACTGCTGGGTTGGGGAGCAGTGGTAGGCAAT[C/G]TGAGATTGCTTT CCTACCCCTCTAAATGTATCTTNTAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCCTGTAAGNTGTTT
WI-1307	118 T C ---			GACAAAGGTGGTACTAGTTCCAAATCCAAATCTATGTACACTTCTCCTCCTCAAGTGGACA GATTTCTGCATTATACTGCTGGGTTGGGGAGCAGTGGTAGGCAAT[C/G]TGAGATTGCTTT CCTACCCCTCTAAATGTATCTTNTAATATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCCTGTAAGNTGTTT
WI-1325b	169 T C ---			GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGCAACCNCTCTGTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCT[C/T/C]ACCCCTCAGAACTTCTTGAGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---			GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGCAACCNCTCTGTGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCT[C/T/C]ACCCCTCAGAACTTCTTGAGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---			CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAGAAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG[T/C]GAAGTTGGTAGCTACCAAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175 C G ---			CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAGCTGTGTAGTGCAGAAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAG[C/G]TACCAAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136	G A ---	---	TATCAGCATGATTGTGGCTGTGGACACAAAGTCAATTTGTACTTTTGNNGNNNTCCCTTTCTNNTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTTNAATATACCCCAAGC [G/A]GGATTGTGATGGATCTGTTTATTTTCTGTGTCTTGAACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCAAGCCACTTGCACTTAGCAAGTGT
WI-1349e	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349c	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1349	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAAAATA
WI-1403b	57	C T ---	---	TGGTATTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTTCTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCAAGTGCCAAAAGGGTTGATCTGATTGT
WI-1403	58	T C ---	---	TGGTATTGGAATGGGTTTCAGACTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTTCTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCAAGTGCCAAAAGGGTTGATCTGATTGT

WI-1417c	31 C T ---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGCGGCGAGATGTGAGCCACGGG GGTGACAGCATGCCCTGCTGGCAATTTGGAGGGCCCCAGAAAGAAATCCAGTGGCCCTCTCAATGACTTG GGTCTCTGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGGTCCGGTTTGGAGCGGTTGC AGCGAGGCCCTTAGGTCGTATTTAATGTTTGTCTTTGTAGAAAAATCGC
WI-1417b	31 C T ---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TJTTGGCCAGGGCGGCGAGATGTGAGCCACGGG GGTGACAGCATGCCCTGCTGGCAATTTGGAGGGCCCCAGAAAGAAATCCAGTGGCCCTCTCAATGACTTG GGTCTCTGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGGTCCGGTTTGGAGCGGTTGC AGCGAGGCCCTTAGGTCGTATTTAATGTTTGTCTTTGTAGAAAAATCGC
WI-1729	172 A ---	---	CCATGAGCAACAGCATGTTCTACTCTGTGATGTATGTTAGGGGCGATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGTATGTGTCCTCCGTGGTNAOCTTCTCTCCACCACCTGCTGTTTTT
WI-1732b	122 T C ---	---	TGCCTTACTTCTTTGTTCAATCCACCATTACATTTGTAAATGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCTTT/CJATTCAAGTCT CTGCCACATGCTAGTAACGTGAGTGATGGTGATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCAATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	TGCCTTACTTCTTTGTTCAATCCACCATTACATTTGTAAATGGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGGAGTNTCCCTGGGT/CJAAACCTTTTATTCAAGTCT CTGCCACATGCTAGTAACGTGAGTGATGGTGATCAGTATATCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCAATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCCCAAAAAGGTTTAAAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGJ/GJTTAAGGTGCTGTTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAAATCTACJ/GJTAGGCGCTTAACATTTTGGCTGAGTATTAATC TGACATGTGTAAATGTGAACCCACCATGAAGCTGGGCAAAAGAACAAATTCCTAGGAAAGTACAATTAC TGGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAATAATCATAAAAAT
WI-1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTTCAGGCAGAA CCATTATGATJ/GJAGTAGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCAGTCTCTAGAAAATCTTACTTACTCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATACTGGAATCA

WI-1803b	77 A G ---	---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTCAGGCAGAA CCATTATGATAGAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGNAGATATCCTG GGTGCTAATTTCAAAATATACTACTAAAGCATGACTCTAGAAAATTACTTATTACTCTTGTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATACTGGAATCA
WI-1837b	112 C T ---	---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAITTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATACIC/TTCGTGCCCGAGTTATTTTT AAGGTTTTTTTTCATTGCACTGATGCCAAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACGTTTAGCTTTCTGCTGGCT
WI-1837	112 C T ---	---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAITTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATACIC/TTCGTGCCCGAGTTATTTTT AAGGTTTTTTTTCATTGCACTGATGCCAAAACAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGAACGTTTAGCTTTCTGCTGGCT
WI-1840b	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TGGAGAACTCTGAATATTGAGACATACAAAGTGTGACACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACTG/TGGAGAACTCTGAATATTGAGACATACAAAGTGTGACACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	---	GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCCTTCTTTTCATAACTACTCCCCG CACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTTA/C/TGCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGCACCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	---	GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCCTTCTTTTCATAACTACTCCCCG CACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTTA/C/TGCTGCNAAATAAACTCCCAAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGCACCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	---	TGTTCTGTGGTCCAGGACCGGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGNTACCTNGGCAATTAGCCCCATCTACAGCTGCAAAAGAGG/C/TGCTCTGAGAGGT AAAGTCCCTGCCCAACGGCAGCACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTCCCATGAGAAACCACTTTCTTGTCTC

WI-1900	119 C T ---	---	---	TGTTCTCTGGTCCAGGACCGGGCTAAGTCTTGCTGATAATGAATAATCAACTGGACAACCCCNCG CTNAGGTAGNTACCTNNGCAATTAGCCCCATCTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTCCCTGCCCAACGGGCACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTCAGATCTGTGTGCTTAAGTCCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165 C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGGTCCCAACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943b	165 C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGGTCCCAACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1943	164 C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGGTCCCAACGTGGAGATAGTGAA TACAGGGCACCCGNTGAGCATTCCAGATGACTCCAAAGCCCGGCTGGAGTAT
WI-1960c	270 A T ---	---	---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTGGAGTGAGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCTGCTGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 A T ---	---	---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTGGAGTGAGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCTGCTGGTTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203 T C ---	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTGTTTTTAGTCTCGTAATAATACTGTTGCCCTAGGAAGGTGTT TTCTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT /C/TAAACAATCAACACTGGCTGAGGCTGTGG
WI-2012	102 T C ---	---	---	AAATTCAGAACCCAGAGTCAGCTCACGATTTATAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCCTTAATTCTGCACAAAACCTAGCTAAAAATC[C/T]TTAAATCAGTTACCAGAGGCAATACCT GGGTAAATGTAAAGCACCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACATTTTTTCTACTCTCAT GGCTTCAACCAATGCTTCCACTGGATC

WI-2013	127 C T ---	---	CTTTAGAGGTGGTCATTTCCGTTCCCTTCTGGAAAGTGATTCGTTTAAAGAAAAATAGATGCAACG TTGCTAAGTAGACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACITTTTGTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGATATCTCAGCTTCTGAGCCCCCTGGTTACTGCAATCC
WI-2032c	166 G A ---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTATAATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACACG/AJTGTTGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATTTGGTTAGGCTCACCTTCCCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2032b	219 C G ---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTATAATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GJCTTCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2032	219 C G ---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTTCTTNACTTACTATAATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACC ACATCACCCAACTGGTTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GJCTTCTGTAATTGCTTCTGTTTTTCAAAAGGG
WI-2054b	188 C T ---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCT/CJ/GTTCTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2054	183 T C ---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGCTTTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCT/CJ/GTTCTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2573d	129 T C ---	---	TGGGATTAACCCCTGTTTCTTCTTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTTGCCGTTTCAAGGTGTTCCGTGCTTT/CJ/GA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCCTAGGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTAAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 A/C ---	---	TGGGATTAACCCCTGTTTCTTCTTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTTGCCGTTTCAAGGTGTTCCGTGCTTTTATAT CATCTGATCTTCCCAACCAGGGCTTATTT/CJ/GCCTAGGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTAAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG

WI-2573d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAATAAGCTTTAAATGCACCTGCCGTTTCAAGGTTTCCGTCGCTTT[C]TGA TATCATCTGATCTCCCAACCCAGGCTTATTTATGCCTAGGTAGGGTAAGCAACACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAATAAGCTTTAAATGCACCTGCCGTTTCAAGGTTTCCGTCGCTTTTGTATAT CATCTGATCTCCCAACCCAGGCTTATTT[C]TGCCTAGGTAGGGTAAGCAACACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAATAAGCTTTAAATGCACCTGCCGTTTCAAGGTTTCCGTCGCTTTTGTATAT CATCTGATCTCCCAACCCAGGCTTATTT[C]TGCCTAGGTAGGGTAAGCAACACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2573a	129 T C ---	---	TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCGCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAATAAGCTTTAAATGCACCTGCCGTTTCAAGGTTTCCGTCGCTTT[C]TGA TATCATCTGATCTCCCAACCCAGGCTTATTTATGCCTAGGTAGGGTAAGCAACACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGGACGAG
WI-2868b	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTCTTAATTACAGACATTAAAGCAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGCTCTTAATTACAGACATTAAAGCAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAACGCTTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131 T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCCATTTTAAATTATATCAGAGCTTTATGTCCTACTTCTCTGTCCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT
WI-2870	131 T C ---	---	CATGCTGTGTAACCTCTGTGCTGCTGCGGGGAAATTAGAGCAAGGAATTGTATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCCATTTTAAATTATATCAGAGCTTTATGTCCTACTTCTCTGTCCTGCCATCAC TGGGCTTTTACAAAGGAGGCTTT

WI-2954c	49	T A ---	---	TTAGCACACATATCTGTGTGGGACTTAAC TGAGACAAGGCATAAAAA/T/AJAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41	A G ---	---	TTAGCACACATATCTGTGTGGGACTTAAC TGAGACAAGGC/GJTAATAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38	G T ---	---	TTAGCACACATATCTGTGTGGGACTTAAC TGAGACAAG/GJGCATAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATTAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62	T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTCCAGTTAGACTCACCAGCATTTCTAAGA/T/CJG CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGAACCTCCTCTCCTTAATAAACCTAAC ATTTCCCTTTGTCCTCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCCTTAATGTATTCTGAAAGAAAACCTTTTACTTAGGGATTGTC
WI-2971	62	T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTCCAGTTAGACTCACCAGCATTTCTAAGA/T/CJG CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGAACCTCCTCTCCTTAATAAACCTAAC ATTTCCCTTTGTCCTCCCTGACATTCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCCTTAATGTATTCTGAAAGAAAACCTTTTACTTAGGGATTGTC
WI-2995d	133	A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGTTTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151	G C ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTGTTTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133	A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGTTTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151	GC	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA AATCTTCTTCTCTGGTG/CJTTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133	AT	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA /AAATCTTCTTCTGGTGTTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151	GC	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA AATCTTCTTCTCTGGTG/CJTTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995b	151	GC	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA AATCTTCTTCTCTGGTG/CJTTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995a	133	AT	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGAGCTGGANTTTTTTNA /AAATCTTCTTCTGGTGTTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-3147	85	CT	---	---	GTGGTGCAGTTCATCCTCTGGAGTCCCTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAG ATCTCACTTAGCTCCTT/CJCTGGCATATCCTGTTTTCTTACTCTCTATCTCTGAGACTTCTTCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTNNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACITTTGCAAGG
WI-3234b	68	TC	---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATTTCTTTATTGAGGTCCATGTCCTTACTCTACTTA T/CJGACAAGCAAGAAACAACAAGCAAGAAAGCCCTGTGTTGCAATCTGGCCTCTTATAAATACITTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68	TC	---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATTTCTTTATTGAGGTCCATGTCCTTACTCTACTTA T/CJGACAAGCAAGAAACAACAAGCAAGAAAGCCCTGTGTTGCAATCTGGCCTCTTATAAATACITTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAAATTCAGAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT

WI-3292b	106	G A ---	---		GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCCTTAAAGGATANTTAGCTCTGCACATCC TCCCTGCCCCGCCAAGCCTATGTTACTGATGCTG/GA/JTGGTATGGATGGGATGGAATTACTT GCCATGAATATTTTCCATTGTTCTCATTAAATGATTAATTAATTAAGTAAATATATTNNCCATGA GACACAATGGAAAAATGGAAAAACATTCATGGAAAAAACCCCATTTCAATC
WI-3292	106	G A ---	---		GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCCTTAAAGGATANTTAGCTCTGCACATCC TCCCTGCCCCGCCAAGCCTATGTTACTGATGCTG/GA/JTGGTATGGATGGGATGGAATTACTT GCCATGAATATTTTCCATTGTTCTCATTAAATGATTAATTAATTAAGTAAATATATTNNCCATGA GACACAATGGAAAAATGGAAAAACATTCATGGAAAAAACCCCATTTCAATC
WI-3355	19	G C ---	---		CCATGAACCATGGGCTAC/G/C/JATATTCCTAACTTCAGAGTCCCTCCTACTGGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTTCCAGCACTTAAACTCATCAGAA AAAAAATCATCAAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A ---	---		CCATGAAGATGAGTTCCTCCCTCCCTGGGTCAGCTAAGAATAGCACACCCCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTCTAAGACACACCTTTATGCTTTCNAAGCTTT CTGGAATGGGATGAATCTNACATTCATATGTCACCCCTCGTGTGGATCATTCTCC/GA/JTGCCCC ATCTCGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	G A ---	---		TAACTTATGCCCTCATCTGGCTTACTGCTTAGTTCCTTCCCATTTGTCATCAGTGCACTTAAAAATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANNGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3505	131	G A ---	---		TAACTTATGCCCTCATCTGGCTTACTGCTTAGTTCCTTCCCATTTGTCATCAGTGCACTTAAAAATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANNGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3564b	177	C T ---	---		GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACATAATGTTTGGAAAAATAAAGT GAAAAATCAATGTGTCTTCCAGTGATTCACATGGCACAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGTTGACTAACGTTAACATGCATGCTGTTC/JAACAAAGTGTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTTCAAAAAACAA
WI-3564	177	C T ---	---		GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACATAATGTTTGGAAAAATAAAGT GAAAAATCAATGTGTCTTCCAGTGATTCACATGGCACAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGTTGACTAACGTTAACATGCATGCTGTTC/JAACAAAGTGTGTTGGTGTGTCATC AGTGTACACATGCTACCTTCTTCAAAAAACAA

WI-3649	64 A	---	AATGTCATGCTGTGACTGACCTGTCTAACACCTTTCTCTAGTATTCTCTTAGTGGAGATTAC[A/G] AGACCAGTTTGCCTTCACTTAGTAGGGCCAAATGATAGACTTTTAGTGCTACCACAAAGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAAGGACCTGTCTAGACTCTTCTGCCTGCCCTTGGTC TTCTGTTTTAOCATATTAAATGATGACATGTCAAACCTCAGAGCCCTTTTA
WI-3674b	133 G	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGGGAGTGCTTTTATAGTAATTAATAATGTTTATTAGAAAATAACAAAATG /CJAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTGGTCAAAATGATTGT AATCTTAATTAATTGTTTTATGTTTNNATTACTGCCAATCAGAGCCAAAG
WI-3674	133 G	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACCAGGGGAGTGCTTTTATAGTAATTAATAATGTTTATTAGAAAATAACAAAATG /CJAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTGGTCAAAATGATTGT AATCTTAATTAATTGTTTTATGTTTNNATTACTGCCAATCAGAGCCAAAG
WI-3682	137 G	A ---	CAATATAGACCAAATGACTGCCACAAGAGAAAATTAGTGGATCTACATTTAGAAAACCCACATGTTTT ATTGGCTCTCTCTTCTCTCTCTCTTTTAAATGCTCTCCAAACCAATTCACTTTATTCTTTTCAA T[G/A]AGCATTTGTCCAAATTTAAAGTCAATGAAAAAATAATGTACATTTTCAACAAGTATACATTAA GCCCTGCAAAAGTCTTATATGCTAT
WI-3854b	194 G	A ---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGGA CAAAGACCAAGGACAACCTGAGGACTTCTGCATGGTCTACCTCACITTAGGCTTCTTGATTAATAACTC TGTTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACCTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194 G	A ---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGGGA CAAAGACCAAGGACAACCTGAGGACTTCTGCATGGTCTACCTCACITTAGGCTTCTTGATTAATAACTC TGTTTCAGGAAGGCAAGGGCAGTTATGACCACCTTACAACCTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210 G	A ---	AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCCATCTCTTATTTCTCTACTGCCTTCACCTT CCATTAAACAAGAACTCTTGATTACATGTATGTTTGGTTACACTACAGAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTAACACCTTAATCTATTGCAATCTTTGTCAATTACCATTAACATATT CATGG[G/A]TTCTGGGATAAGGGGTAGACATTTTTATGGGAGGCCATTA
WI-4110b	130 T	C ---	GAAAAATGATGTTTTGATTTCCCTTCCCTATCTTCCAGATTATTGGAGTGCTATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCCTCTCTCTTATTTTGGCTT[C/J]ACA GTTTAGGTAATAAAAGATGCCAAGAAATTCAGTATTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGGAGGAGGTGGGGGTTTTCTGGGAAGA

WI-4110	130 T C ---				<p>GAATAATGATGTTTTGATTTCCCTTCCTATCTTCAGATTATTGGAGTGTCTATTAGAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAAACCTTCCTCTTCCTGCTTTATTTTGCCCT/CJACA GTTTAGGTAATAAAGAGATGCCAAGAAATTCAGTATTCAGTACAGTAAAGAGTACGAAACCATGGG GTAGGGACAAGTNCAGAAAAGGGAGGAGTNGGGGGTTTTCTGGGAAGA</p>
WI-4119b	168 G A ---				<p>ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACACTACGGGGAAGAACAGGACAAGAACAGACAGACAAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA/G/AJCAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTCA</p>
WI-4119	168 G A ---				<p>ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAAGTAATAAATAG AATGGAAGGATAAATAAAGGTAACACTACGGGGAAGAACAGGACAAGAACAGACAGACAAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA/G/AJCAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTCA</p>
WI-4123b	51 T G ---				<p>CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAATAGAAAAGTG/T/GJTTAAACTATTT CAAATAAACAAATAAAGAAAAACATGATGAAATTCCTCGTTACATAATTTGTATAGAATTTAGTGGG TTCCTCCATGACATTTGGCTTGTCTTCTCTCAACAGTGGGTGGTTGGATGTTTTCCATGCTTTCTC AGGCACAAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG</p>
WI-4123	51 T G ---				<p>CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAATAGAAAAGTG/T/GJTTAAACTATTT CAAATAAACAAATAAAGAAAAACATGATGAAATTCCTCGTTACATAATTTGTATAGAATTTAGTGGG TTCCTCCATGACATTTGGCTTGTCTTCTCTCAACAGTGGGTGGTTGGATGTTTTCCATGCTTTCTC AGGCACAAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG</p>
WI-4149b	145 G C ---				<p>TTGTACATGTTCAITTCATCCCTCCCATCTTTCTGTCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTTCTCAGCATCTCTATATACT GTGCTG/G/CJCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGCTTGAACGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG</p>
WI-4149a	137 T C ---				<p>TTGTACATGTTCAITTCATCCCTCCCATCTTTCTGTCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTTCTCAGCATCTCTATATACI T/CIGTGTGTGCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGCTTGAACGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG</p>
WI-4182	188 G A ---				<p>TAAACACACTTTTCATTTGGTTTCTATTACTGCAGTTAAAGGACCATCCATTATTAACAATTCCTC AGTTCTATGCTTTAGAGTNCATTAATAGGACTACTGTAATAATTCAGAGGAAATTAACCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCGAGGGACTGTGGTTAA/G/AJATGTCCTCTCT TGCCCCCTTCCCAAGTCTTAATTCCTAG</p>

WI-4230	93 T	---	---	AGAGACGTTGAATGGGGACATCTTTCTATTTTCGATTTAGTTTAAACATTTGATAAGAATTGATGAAA GTTTGTACATCCAGATTTATCTTTATAGCAGCAGAGTCTGGCAAATAAATACACGACACATGACT TTTCCATGGTAAAGAAAGTTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATTCGAAAT ACATTTAAATGGAGGAGATGAATAGTGACCTTTGAAATTTGAAATTTATGG
WI-4241	118 C T	---	---	GAAATTCATTTGAAGTTTGAACCTTGAACCTGATCTCATTAATACATTTTNCCTGTAGTGGTTGATTT CATTTTGTACAACAGAACAGACGAAATTTCCACTTAAATTAATCTC[C/T]AAGTATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTTATCTCTAGATATCTTCAGAACTCTAGGATGGAAG AA
WI-4271b	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGAATATTAGAGTACTACAGGAGCCCCCAACCCCTCCCTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGAATATTAGAGTACTACAGGAGCCCCCAACCCCTCCCTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A	---	---	AATCGAAACATTGATTTTTTTGTAAAGGAACACATTTATGATATTTTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]JNCGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4389	156 G A	---	---	AATCGAAACATTGATTTTTTTGTAAAGGAACACATTTATGATATTTTGCCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/A]JNCGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4488	31 A G	---	---	GATGACAATTATTGTGATTGGCATTTTAA[A/G]GTACCATTCCATTTTCTCTGGCTTTCGTGTGT TGTTGTTGAGAAAGTCAGGGTTAGTCGTATTGCTCTTTTCTAGTCTTCTCAGTAGGAAGACTGATC CTAAACAACTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C	---	---	ACCATCAATGTATCACCTTCTAAAAATTTATTAGATGATTAACTGGCTCTGTTAAAAAATAAAAAACCT GTCCTGGACATTGAAAAATAAACATTAATACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACTA AACAAAGTTAAG[G/C]GTTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACTGTCA TTTCTTGTCCTCAATAAATAAATTTTACATGCCT

WI-4584	144	A G ---	---	TTGGTGGCATTTAGCCTCATAACAACTATTACAATCATATTTACTCTTATTTACAAACAAG AAAATGAGGCTTAACATCACACTCTGCTTAGTCGAGAGCCAAAGATTTGAACCCAGGAATCCATT CACCGGTACAGJTGCTACCTGGTAAAAAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGTTTTGAAAATAGGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185	C T ---	---	TTTCTGCATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCAATTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[CT]CACTCTTTAAATTTGTA AATTTTAAGGACACCTATCATAGTAATAATTGTGAGGATAAATGAAATAA
WI-5327	63	A ---	---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGAGGATGGTGGCTGAGAGA[A/- JGATTAATCATAAAAGCATATTAAATTTATAAATATGAAAAATTTAACTAGATAAATTAATGTAAT TGAGTTTGAAGTTGCATGAGAGTAGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCCGATGACAATGATGAATGTTCTAAAGCAGACAG
WI-5390	87	C T ---	---	GCCTTTGAGAAATGAAAAGGGGAGCCTGGACCAATTCAGAGGCTTCTCATCTCTGATATTTTGTGTAT TTATTGTTCACTTATTAT[CT]GCTGCTCTCCCTTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCAGTGCCTGGCCGATTCGTGGCTCTAGAGGTGTCAGAAAAAAGTTTCCGTGAATAGAAATTG ACGAATGGTTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCTCTCAAGAAATCAATTTAAGCAGT GCAACATTATTTAATTT[G/A]AAAGAAACCTGTTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTCAACAA
WI-5404	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCTCTCAAGAAATCAATTTAAGCAGT GCAACATTATTTAATTT[G/A]AAAGAAACCTGTTCTGAAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTCGTAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTCAACAA
WI-5545b	77	A C ---	---	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATCTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCCAACACCTCTGTTTCTGACAGCCAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
WI-5545	77	A C ---	---	TAGGAAAGGGGATGGTGATGGCCTCTGAGACATTTAAATCTATCTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCCAACACCTCTGTTTCTGACAGCCAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA

WI-5860b	134 A G ---	---	---	ACTCAAGTTGGGGGATAAAATCAGAAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGTTTCTTTTATATAAAATATGGATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC[AV GJTTACTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	---	ACTCAAGTTGGGGGATAAAATCAGAAAGTTTCTATGTACAACTTAAATTTTGCTAAGATTTTATTGTTTCTTTTATATAAAATATGGATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC[AV GJTTACTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	---	GCAACAACCTATTATACCTGATTCCAAACCCAGGTCTACTAACATTAAATCAACCCCTAACCCACAATAC TATATATTGCTCCTGTTCTGAATATTATTTCAATTTAGAACTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGGCTTCCAGGAGTCTCAATGTGAAGTATAATTTCTTACAGAG TAATTC[CG]ATAGTAGGTCAACCAAAAGTCTATATTGTATGTGAAGGAAAAG
WI-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTTC[AAACCCCTATATTNCTGCTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCCTGAAAAATTTTATACCA
WI-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTTAA ACCTATATTNCTGTC[CG]TTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAAATTTTATACCA
WI-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTTAA ACCTATATTNCTGTC[CG]TTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAAATTTTATACCA
WI-6109a	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAAAAACCTTC[CG] AAACCCCTATATTNCTGCTTGTGCATACITTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCCTGAAAAATTTTATACCA
WI-6112	96 T C ---	---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGATTC[CG]CATATCCCAAGTCCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTGACTAAACATACITTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103	T C ---	---	TAATTGCACAACCTACATAATCAGGGTTTCTGATTGAAGGAAGAGAAATATTCCTTTCTTTAGTGATT GCTTAATAATTAAATTAAGTGCACCATCTCTT/CJGCTCCTTATAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACCAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTTCTTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	C T ---	---	CTGGCCTTATAATCCAAGTTTAGGATTAACTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCTCCTAGTAGGGCTTTGGGTGGCACCCTTTGGCTCATTC/C/PIACTCTCCCT GGGTCTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTCCAAAGATTTCGTTACGATTTTATA
WI-6336b	234	C T ---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGGCTGAGAGAGCTCACTCCCCC ATATATTTCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACCTGGCAATATATTACAGATGGTTTATGTACAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCAATTATGCTTGGTAGAGCC/C/TJTGAGGACACTGCACAGT
WI-6336	234	C T ---	---	AGGTGCCATTAAATCCATTCAAAATTTGGAAGCTACATCTTCAAGGGCTGAGAGAGCTCACTCCCCC ATATATTTCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACAACTAAACAGCTT ATATACCTGGCAATATATTACAGATGGTTTATGTACAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCAATTATGCTTGGTAGAGCC/C/TJTGAGGACACTGCACAGT
WI-6381	92	C A ---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNNITTCATGTTTAAACAA/C/A/GTATTTTAAAGCTCAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGCTTTTGAATGTCTCTCACTCCCACTTCAACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
WI-6436	198	C G ---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTAGGGCAGTAGAANAATGGACATTTTAGGAAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAGTTTAGACTTTGGTGGTTGAGTAGTTGAGTAGGAGTAGCGTT/C/ GIATTGGGTGATTTCCACAGACAAGGTGATGTTCTAAGATTGATATTATTGT
WI-6449	186	C T ---	---	GAGGCCTTTTGGCTTTCCCTCAGTCAAGGCTGATCCAGGGTTGATATCTAGCCATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTGCTCACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTCTATTCACTGCAATCTCTGATCTTATGCTGGCTCTATT/C/PIATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAATTTTCTGGGTGATTATA
WI-6449	186	C T ---	---	GAGGCCTTTTGGCTTTCCCTCAGTCAAGGCTGATCCAGGGTTGATATCTAGCCATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTGCTCACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTCTATTCACTGCAATCTCTGATCTTATGCTGGCTCTATT/C/PIATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAATTTTCTGGGTGATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAAAGAACTAAATCAGAGTCCTTGAGCAAGAGGAATTGAAA AGAACATTCJTGAAAAAATTAAAGTAGAACTCAAGAGCCAAAAAGTCCCAATTGTGTCCATT TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCCTCCTC CAGTCCCATTTATATGACATCCGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAACJTGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAAGGGGTGCTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAAACJTGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTGAAAGGCACAGAGAAAAGGGGTGCTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACTCAATTAACCTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCCCTCCCAATAGTGAGAAATCAGAGTTAGCTCCTTGTGCTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACTCAATTAACCTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCCCTCCCAATAGTGAGAAATCAGAGTTAGCTCCTTGTGCTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTGAATGCAACTGAGAAANTGGTTTNTAGGCTACCTTTTAAAGATACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAAATTTTAAAGAGAACAGGAAATAAGGAAGGCCCTAACAGAGGAG TTAAATAATTTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATGGTCCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCAATTTGATTATNATTTTGTGTTGGGCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATGGTCCCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTGCTGCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCTCATTNCTCAGAAATGAAGGCAATTTGATTATNATTTTGTGTTGGGCTGTGTAAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA

WI-6608b	46 C	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGGTGGCCTCAGT[C/- JAGTTGAGGAGCTAAAGGAGGGGATTTCTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTCCAGCACACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCTAGCTACAAGGCCACACCAAGAAAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGGTGGCCTCAGT[C/- JAGTTGAGGAGCTAAAGGAGGGGATTTCTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTCCAGCACACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCTAGCTACAAGGCCACACCAAGAAAAAGGAA AGC
WI-6666	68 C A	---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTTCCAAAAAGAGGAAACCTCCCC A/C/AJAAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTTACTCTGTGTGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCTCTCTNITCTCAAGTTCAGGCTTCTGGGTAGACCAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G	---	---	AGATTACATAATTATACTGGGGCCATTGTAGGTTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTAGCCA GCATTGCCATTACAGGGCCGAGTCAGGTTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAATCTTAGAAGGGAT
WI-6670	120 A G	---	---	AGATTACATAATTATACTGGGGCCATTGTAGGTTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTAGCCA GCATTGCCATTACAGGGCCGAGTCAGGTTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAATCTTAGAAGGGAT
WI-6704c	33 T C	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAAC[T/C]CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C	---	---	TTTGAAAATAAATTCATGCACCAATGTTTTAAC[T/C]AACCTACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGACATGTCATCAATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---	---	---	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTAGTAATAACAGAGGAAGTCCAGTTATCTACCT ATTCCCTTAAACACATTTTGTGAGGCTGGAATGATTCCTC[G/A]TAGTAAACCTCAACATCCACACCT GCATAAACATCGCTCCCAAGTGACTATTATTACTGAGTCGACAGGATGTCACCAAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---	---	---	AAACAAATGGTGCTTGCATAATATTGTGGTCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTGTCTACGGAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTTCCTCTCTC
WI-6766	148 G C ---	---	---	AAACAAATGGTGCTTGCATAATATTGTGGTCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTGTCTACGGAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTTCCTCTCTC
WI-6787b	97 A G ---	---	---	ACAGATAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTATACA ATACTTGTGCAGCAATGTTCAAAATTCAC[G/J]TTTTACTGCATAAGATATCTTCATGTACAACCTGT ATGCTTTGTCTCTTGGGAAGGACGGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGCAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	---	GAACCCACAGGCTCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAATCAATCAGTCAACCCCTC[G/G]AGTTAGAAAGTAGATCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGGTTAATGCCCTCTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTCATCACAGGTAAAGGCAAC
WI-6810b	37 T C ---	---	---	CACAATAATAAATCACTCCCTACCTTGAACCTTTAT[C/J]AGAAGCATTTTTTAAATTTACAACACA AAGCTCAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACNGCCAAAGGATAAGGCTGAACAATA AATTAAACCTTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAAGTTCTGCAGAGCAATGACC ACTAAGNAATAATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	---	CACAATAATAAATCACTCCCTACCTTGAACCTTTAT[C/J]AGAAGCATTTTTTAAATTTACAACACA AAGCTCAAACGNACCTACAATAAGTCTAGTAGTCTGTTTACNGCCAAAGGATAAGGCTGAACAATA AATTAAACCTTTAAAAATGTCTATGNACAAGTACAATTTCTTTTGAAGTTCTGCAGAGCAATGACC ACTAAGNAATAATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAAATCATCACTAACAATGTAGCT GCAGGGTAAAC[C/A]JTGTTGATACCTGTGTGCTCTACTNGOCTCCAAAGGCAATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAAGTGGGCTGTGCGAG

WI-6817	145 C A ---	---	GCATGATTAACCAAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGTAAC[C/A]ATGTGGATACCTGTGTCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTTCAATCTTGTTCAAGTGCGGCCCTGTGCAG
WI-6819b	221 C ---	---	GATGAAAGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAACATTTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG CTTTAGCAACAGCAATAACTTTTGTTCTCTATATGACACCTAATATCCAG
WI-6819a	175 G T ---	---	GATGAAAGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAACATTTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTTCTCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	GCAAAAGCTTTATGGTCCCAACAAATTAATCCCTTTTAAACTCCCTCTCTCTCTGGTCTCAGTG GAACAACACATTTGAATTTGAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATAATAATAC ATGCAAAACCTTGACAT[G/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATTATGGCAACACACACTGGGACTGGGTATACGTTG
WI-6826	154 A G ---	---	GCAAAAGCTTTATGGTCCCAACAAATTAATCCCTTTTAAACTCCCTCTCTCTCTGGTCTCAGTG GAACAACACATTTGAATTTGAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATAATAATAC ATGCAAAACCTTGACAT[G/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATTATGGCAACACACACTGGGACTGGGTATACGTTG
WI-6857a	122 T C ---	---	AGTGCAAACTATTTGAACAAAGTAACTATGAGTCACAGCATTTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCCTAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT[C/J]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTCAGTGTAAATTCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153 G A ---	---	TTATAGAATACTTATGGGGCATACGNGTAAATGAACCTGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTTGTTGCTCGTGAATCCTCCCTGCTCACAACACAGCCAGCTACTNGGTTTTCTAAAGACGTA ATTTGCAGGCAAACTT[C/G]ATAGAGCCATTCGTGCGAAGAAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTGAAGATATCTTTGCGCTGTAGAACTGAGCTCATTA
WI-6909	73 C T ---	---	ATTGAAACTGGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAATGAGAGAAGAATGC AGACTTA[C/T]AAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATAC GGAAAAAAAATTTCCCTTTTGGCAACAGGATTATTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATAATTTGCATGCCCTAGTTGCCTATTTTATACATATC

WI-6910b	163 G T ---	---	CACTCAAAACCTTTATTCAATTGATTTACAAACTGTACAATATTTACAAAGTTTGTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGACCTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---	---	GCTTGTTTTTTTGTTTTTTTAAAGTGACACCTTGGCCTTGTTGGCATTTCTTCACCTTATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNAATTTCTATTTGGTAGTATTTTTCAGATTTCCACAAAGAACATG TATTGCTTTGTAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C ---	---	CAATCAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGTAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAGTTCACTCTTAATTTTCATGTCCCATG CTTGCTTGGTCCCTGTGAGGAAAGGGTGACGTAAGG[T/C]AACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGIGACCTTAGAAGTTA
WI-6928	175 T C ---	---	CAATCAAAAGTTCCAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGTAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTGACGTAAGG[T/C]AACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGIGACCTTAGAAGTTA
WI-6955b	79 G A ---	---	TTTTATGAAACATTTCCAGATCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTATAGTAC[G/A]NGTCATGTCCCAAAATCCCAATCCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---	---	TTTTATGAAACATTTCCAGATCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTATAGTAC[G/A]NGTCATGTCCCAAAATCCCAATCCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47 C G ---	---	AAACTAAAAACCCCTATTGTCTCCAGTGTTGGGCAAAATAGAAAAT[G/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTAGTTATCCACTTAAGAAGCATCCAGTCAAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAACTGGATTTGAAACCCACTTTAGG CTAAAAATAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAAATCATGC
WI-6996c	242 G T ---	---	ACTTCTAGTGCCTCTGTTACCACCACCTTAATGCCTCTGGTCGCCGCACTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGGCTCCCTCCCTCTGCTTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGGTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGAACCCCTGTCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTTCTCTCC[G/T]GTCGGATC

WI-6996b	242	G T	---		ACTTAGTGCCTCTGTACCAACACCTCTAATGCCTCTGGTCGCCGACCTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCTCCCTCCCTCTGTCTTACGACCCAGAGGAGGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGTGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTGACT CTCTCTGATGGTGGCCCTCTGTGCTCTTCTCTTCCG/GTGTCCGATC
WI-6996	228	T G	---		ACTTAGTGCCTCTGTACCAACACCTCTAATGCCTCTGGTCGCCGACCTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCTCCCTCCCTCTGTCTTACGACCCAGAGGAGGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGTGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTGACT CTCTCTGATGGTGGCCCTCTGT/GTGCTCTTCTCTCCGGTCCGATC
WI-7021b	112	G A	---		TGGGAGGACAGGGAGATGCTGCAGTTCCAAAAGAGAAGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAAATATGGTCCAAAT/GA/CCCGACTGCACCTTCTGTG CTCAGCTCTTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---		TGGGAGGACAGGGAGATGCTGCAGTTCCAAAAGAGAAGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAAATATGGTCCAAAT/GA/CCCGACTGCACCTTCTGTG CTCAGCTCTTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	---		GGCAGTAGGACCAACAGTGGGGTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTCTCCAAAGTTCCAAACACAGAAAGTCATTCCTCTTTTAAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	C T	---		GGCAGTAGGACCAACAGTGGGGTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTCTCCAAAGTTCCAAACACAGAAAGTCATTCCTCTTTTAAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C	---		AATTCGCTGAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAAGGCATATGGAGAACATGTTTATACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATT/C/CTTATCAATTTATCAGCCTTTATGTATTTTCCAAAGTAAATAATTA ACATAATTATTCATTGGTCTCTTTTATCTGGTCTATATGAATGCTAT
WI-7091	153	A/C	---		AATTCGCTGAAAAGGAACTACCTATCCTTACATTCACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAAAGGCATATGGAGAACATGTTTATACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATT/C/CTTATCAATTTATCAGCCTTTATGTATTTTCCAAAGTAAATAATTA ACATAATTATTCATTGGTCTCTTTTATCTGGTCTATATGAATGCTAT

WI-7136	58 T C ---	---	TGTGAAGCCACATTTTCCAAACATGAGCCTCATGAAGCCAACTAAGTGTATTGAACCTGTTCJAATTC TCTCAATAACTCAGTGTAGCACCTTTAAAGTCTGAAGGACAGCAACATGAAAGAGCATATCAATGTG GTGGAGAAAGGGAAGGGTGGCTTTTAAATTTATTTCTTCATCTTTTATAACAGAAAGNNNN NNNGTAGCTTCTCTATATG
WI-7146c	210 A G ---	---	GGGACGCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGCCCTCTCGGCATGOC AACGC[A/G]GTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210 A G ---	---	GGGACGCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGCCCTCTCGGCATGOC AACGC[A/G]GTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202 G A ---	---	GGGACGCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTCCATTTTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTCTGTTGCCCAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGCCCTCTCGGCAT[G/A] JCCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161 A T ---	---	ATATTACAACTGCTTTTAGCTGATCTCCATCTCAAAATGACTCTTTTCTTTATATGTTAACATA TATAAATGGCAACTGATGTCATTTTGAATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNNN[A/T]AAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAATGGTATGTTT
WI-7155	156 T G ---	---	TAGAATAGATCGGTCATATTCTCTTGGCTTCTGGTCTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACACAGCTGGCCCTACCCCTAATATGATCCTGTGCTCTAAATTAATACAC CAGTGGTTCTCTCTCCCTGT[G/T]AAAGACTAATGCTCAGATGCTGTTACGGATATTTATATTTCTAG TCTCACTCTCTGTGCCACCCCTCTCTCTCTCCCAATCCCACTCCAG
WI-7169b	161 A G ---	---	AGCTCCACAGATGCAGATTGTGTTTGTGTTTCTGTTATCACTGTCACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGTCTAGCCCAAGCCATCAAGTGTCTGAAATTCAAATTTGGTTTATGCAAAT ACAGCAAACTTTTATTTAAGTAGAT[G/G]GGAGAAATATGTTTAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATTCTCAAAATGGAAGTTATATATA
WI-7175b	194 C T ---	---	CTCCTAGACTAGTGTCTTACCTTTTAAATGAACGTGTGACAGGAAGCCCAAGGCAGTGTCTCACCAC ATAAATTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGTCTGTCATTTGCTCCATGCCTA[C/T]JAGAT AATTTATTTTGATTTTGAATAAAAAACATTTGTACATCTCTGATCTGGG

WI-7175	194	C T	---	---	CTCTAGACTAGTGCCTTACCTTTATTAAATGAACGTGTACAGGAAGCCCAAGGCAGTGTTCTCTCAACA ATAACTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATAATGGTTTACTGCTGTCATTGTCCATGCCTA[C/T]AGAT AATTTATTTTGATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273	G A	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGCTCTAGGGGAACAGACCAGTGACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTTACGCTGAGCCCTGGGACTGTTCAAAGCCAGTGAATGTGAAGGA
WI-7178	273	G A	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGCTCTAGGGGAACAGACCAGTGACCCAGAAAAGCATAACACCA ATCCAGGGCTGGCTCTGCACTAAGAGAAAATTGCACTAAATGAATCTCGTTCCCAAGAACTACCC CCTTTTACGCTGAGCCCTGGGACTGTTCAAAGCCAGTGAATGTGAAGGA
WI-7182b	116	A C	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCACTCTGAGCCT[A/C]TCTCTCCTCCTATTT TACTTGAGGCTGCCAATTACAGCCCAAGTTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCTTTGGTAGCAAGAATGGCAGCTATTCTCGAAGCCTAGTACCCCAATT
WI-7182	106	C A	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCCA[C/A]TCTGAGCCTATCTCCTCCTATTT TACTTGAGGCTGCCAATTACAGCCCAAGTTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCTTTGGTAGCAAGAATGGCAGCTATTCTCGAAGCCTAGTACCCCAATT
WI-7191b	273	T A	---	---	ATAATTGCTGTGTTTCTAGCCTGGCAAGATATTTTCATAAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACCAAGCACCATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACCTAGAAACAATGAAGCTCTTGGCATATTTTAAAGGAG CTCCCAAAATGTTACCTATTAAATTGTAACTCAGCAAGTAGAAGACCATT
WI-7199c	112	T C	---	---	CCCAAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCTTCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTACGCTCCTTGACCTATGAGCT[C/G]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCTCAGTTCTCACCATCATCTTGCTAA
WI-7199b	112	T C	---	---	CCCAAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCTTCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTACGCTCCTTGACCTATGAGCT[C/G]GGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGTTGCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCTCAGTTCTCACCATCATCTTGCTAA

WI-7216c	237	T C ---	---	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCTTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTTTTCCTTGTAATCACTT
WI-7216b	237	T C ---	---	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGTCTTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTGTTTTTTCCTTGTAATCACTT
WI-7220b	147	A T ---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCAATATTGTCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAJA/TJAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATAATTAGTGTGTTT
WI-7220	140	A T ---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCAATATTGTCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCA/TCTAGAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATAATTAGTGTGTTT
WI-7226	232	C ---	---	GATCGAATTTTTCAGATGATTCGGAAATTTTCATTCAGGATTTGTAATAGTGACATATATATGTATA TACATATCACCTCCTATTCTCTAAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATTT CCCTTTCCATATAGGAAACATAAATTTGAAGTGGCCAGATGAGTTATCATGTGAGTGAATAATA TTACCCACAAATGCCACCAGTAACCTAACGATTCCTCACTCTTGGGGTTT
WI-7228b	254	G A ---	---	ATAGCTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCAACAGGAGATTACAAATTTTGTCTCTTCTGCTCTTGTAACTCTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGGATCAGAAGATATCTTTTGTGCCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAATAAGAAATGTTATCCAACCTATTAAGATATCTCAATGTT
WI-7228a	163	G A ---	---	ATAGCTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATGGCTCCAATTCATAA TATGTTCAACAGGAGATTACAAATTTTGTCTCTTCTGCTCTTGTAACTCTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGGATCAGAAJG/AJATATCTTTTGTGCCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAATAAGAAATGTTATCCAACCTATTAAGATATCTCA
WI-7233c	213	C T ---	---	CGATCGTACTGCCAGTAGCATTTGTCTGTCTGCCGGCTTGTGTGTACATTCATTTTCAATTTGATACA GATGTGAACITTTATCTTGTCACTAATTAATTTAAATTTTCTAGGAAGTCAAAAAAATATAA TAAAGGTTGAGCCCTCTACTTTCTTCTTCCACCTTTTGTGGCAATATTAAAGTGAAGTACTGCTAATA GTGTAAGTAJCTGTGCACAAAAACCACTGCCAGATAACCAAGAGGGGCTG

WI-7233b	213	C T	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGGCTTTGTGTACATTCATTTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACTAATATATTTAAATATTTCTAGGAAGTCAAAAAAATATAA TAAAGGTTAGCCCTCTACTTCTCTTGGCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAGTAC/TJGTGCACAAACCACCTGCCAGATAACCCAGAGGGGCGCTG
WI-7233	211	T C	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGGCTTTGTGTACATTCATTTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACTAATATATTTAAATATTTCTAGGAAGTCAAAAAAATATAA TAAAGGTTAGCCCTCTACTTCTCTTGGCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAGTAC/TJACGTGCACAAACCACCTGCCAGATAACCCAGAGGGGCGCTG
WI-7238	128	T C	---	GGTCTACAGACAGCTACCATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTTC/TJCCGTT CTGTTTAAACAGAAATAAAGGAGTGTAGTCTCTTTCTCATTTCAAAGTTGCTACCAAGTGTAT GCAGTAATTAGAACAAGAAACATTCAAGTAGAACAATTTATTGCCTA
WI-7252f	520	T C	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCGGGCGCCAGCCCCGGCCCTGGCTCGGAGGCTGCCCCCGCCCTGGTCTCTGTGTCOG GACACTCTAGAGAACGCGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCCA
WI-7252e	552	T C	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCGGGCGCCAGCCCCGGCCCTGGCTCGGAGGCTGCCCCCGCCCTGGTCTCTGTGTCOG GACACTCTAGAGAACGCGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCCA
WI-7252d	540	T C	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCGGGCGCCAGCCCCGGCCCTGGCTCGGAGGCTGCCCCCGCCCTGGTCTCTGTGTCOG GACACTCTAGAGAACGCGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCCA
WI-7252c	552	T C	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCGGGCGCCAGCCCCGGCCCTGGCTCGGAGGCTGCCCCCGCCCTGGTCTCTGTGTCOG GACACTCTAGAGAACGCGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCCA
WI-7252b	540	T C	---	CCACAGGATCCAGCCCAAGCGGCCCCCTCCGCCCCCTCCACTCGCAGCAGCGCGGGGACAGAG GCCTGCCCGGGCGCCAGCCCCGGCCCTGGCTCGGAGGCTGCCCCCGCCCTGGTCTCTGTGTCOG GACACTCTAGAGAACGCGCCCTAGAGCCTGCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCTCCA

WI-7252a	520 T C ---	---	CCACAGGATCCAGCCCAAGGGGCCCTCCGCCCTTCCCACTGCAGCAGACGCCGGGACAGAG GCCTGCCGGGGCGGCCAGCCCGGGCCCTGGCTCGGAGGCTGCCCCGGCCCCCTGCTCTGGTCCG GACTCCTAGAGAACGCGAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT
WI-7265l	231 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCTCTT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231	T A	---			AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCTTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265e	227	T C	---			AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCTTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCTCT AAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265d	174	T A	---			AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCTTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265c	170	T G	---			AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCTTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265b	121	T G	---			AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCTTCTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7265a	80	T A	---			AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCTTCTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATAGATGCAATAGTATTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGCGCT
WI-7281b	183	C	---			GATACCCAGCCACAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCCTTGGCAAAAACGGAGTCCGCGAGGCCGAG GTGTTGTGAAGACCCTCGTTCTGTGGTGGGGTCTCTGCAAGAAGGCCCTCCTC
WI-7281	171	C A	---			GATACCCAGCCACAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCCTGAGTCTCAGTCTCAGTCTCAGTCTCAGTCT CAGGTGTTGTGAAGACCCTCGTTCTGTGGTGGGGTCTCTGCAAGAAGGCCCT

WI-7282b	159	C ---	---			TGTCACCTGGCACATTCATTTTCTCAGTTGAAGAAGAGAAAAATTTGAAATGTCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCCTCACTCAAATATGTCAACTNNNNNNNT AGGCCCTTTCATAAAAAACCAACT[G/C]TAGCAAGATGCAATGCATGGCAAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTCAACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---	---			CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGTCTCCCAATTATATCTCCCCCACTCCACTAC TCTCTCTCCACTTCAATTTTCC[C]/CTTGTCCTTCTCTCTAATTCAGTGTTTTGGAGGCCCTGACTTG GGGACAACGTATTATTGATATTATTGTCTGTTTCTCTTCCCAATAGAAATAAGTCATGGAGCC TGAAGGTTGCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG A/GJCGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCA ATCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94	T G ---	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/[G]TGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138	A G ---	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGT[A/G]TAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211	A C ---	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAATCA AATTATGGAC[A/C]ATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182	C T ---	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAAT[A/C]/TAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88	G T ---	---			AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGT[G]/TGGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG

WI-7301	205	A C ---	---	---	AACTATGGCAGTGGTCTGGTTATAGTAGTAGAGGCGGTATGGTGGTGACGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGTGGAACTATAATGATTTTGGAAATTACAGTGGAACAACAGCAATCA AATTACJTGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49	G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAATTTGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCTTTTCAGCAGGTGTAATAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACTTGTTTTT
WI-7314b	49	G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTA[G]TTTGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCTTTTCAGCAGGTGTAATAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACTTGTTTTT
WI-7314	36	A G ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTA[G]TTTGGGAGGTCA[G]ATTGTTCTACCTCACTG AGAGGGAACAGAAAGGATATTGCTTCTTTTCAGCAGGTGTAATAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACTTGTTTTT
WI-7321b	199	C T ---	---	---	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCCCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T ---	---	---	AGACATTCTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCOCTGGC TCCAGTGAACCTTGGGCACATGCTCAGGCTACTATAGGTCCAGAAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAATTTCTGAATTTTGGGATTTTCAAAGATAATATTTACATACACTGTATGT TATAGAACCTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7336b	248	A C ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGCAGAGAACAAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCGTT
WI-7338c	221	A G ---	---	---	

WI-7338b	125	A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGTGCAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGTGT
WI-7338	125	A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGTGCAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGTGT
WI-7338	221	A G ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGTGCAAGAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCGTGT
WI-7384c	146	T A ---	---	CCATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAATTTAAATACCATTAATACATTTGATTTTCAATTTGTAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACATTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146	T A ---	---	CCATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAATTTAAATACCATTAATACATTTGATTTTCAATTTGTAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACATTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145	T A ---	---	CCATGTCAATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAAATTTAAATACCATTAATACATTTGATTTTCAATTTGTAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACATTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7388c	106	A T ---	---	TGAAATCCTGGGTCCTTGGCCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTCTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTTGGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGCTGTCCAGAAGCTTTTCCCCCAAGATGTGTATAGTTATGG
WI-7388b	106	A T ---	---	TGAAATCCTGGGTCCTTGGCCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTCTTTT TGAGATCCATCCTTTATCAAGAAGTCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTTGGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGCTGTCCAGAAGCTTTTCCCCCAAGATGTGTATAGTTATGG

WI-7388	94 T A ---	---	TGAATCCTGGGTCTCTGGCCTGTCTGTAGCTGGTTATTTTACTTTGCCCTCCCCACTTTTT TGAGATCCATCCTTTATCAAGAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGATTGTGTTGA CTTGCTGTCTGCCAAGAACTTTCCOCCAAAGATGTGTAGTTATTGG
WI-7438	64 A G ---	---	TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATCCCACTGCAGATCTNCTATTCCTGG[AG] GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTCAGATTGTNCCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCACCTGTAACATAGTTTGTNCTGGTATTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ---	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152 T C ---	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177 G C ---	---	AATTTGAAAATCTGAAAAAAGTGCTAAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTTATATTTCCCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCAACCAAAATTAT
WI-7464b	168 C A ---	---	AATTTGAAAATCTGAAAAAAGTGCTAAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTTATATTTCCCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCAACCAAAATTAT
WI-7464a	103 C A ---	---	AATTTGAAAATCTGAAAAAAGTGCTAAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCTACTCAGTCCATCTTAACCATGTACAAATGCATAAATTAATTTATATTTCCCTAT GTACAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAAGAGCTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCAACCAAAATTAT
WI-7499b	134 T G ---	---	CAATTCCTCAATCCAACTTAGTCTGNTGCCTAAACCATCCAGACAAACCTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGGTTCTTTGAATGCTTCAIT /GJTATAGTCCCTTCAITTAGCAATCAGTGAGGGCAATACACTGGCATCATGCCCTTTTTTTAGGA ACTCTGTACAAAAATCCCTTTTGAAAAATATAAATTTTGAAATGAGTGATGA

WI-7499a	33	A G ---	---	CAATTCTCAATCCAACCTAGTCTGTGTCCTAA/GJCCATTCCAGACAACTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCITTCAGTTGCCAGAGGCACATCAGTTCITTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAATTCCTTTGAAATATAAATTTTGAAATGAGTGATGA
WI-7506b	118	A C ---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGGTGTGATTGCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAATCATGATGTCATGTATGCAGTAATTAATATGTCA GAAGAAAATATTTTAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7506	118	A C ---	---	TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGGTGTGATTGCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAATCATGATGTCATGTATGCAGTAATTAATATGTCA GAAGAAAATATTTTAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143	C T ---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTATGCCCTTGGGGTTCTTGATGTGTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGACACATCCCGGTGATAGAAATTCCT AAATTTGTC/TJGTGAAATAGGTAGAAATTTTCTTAAATTAAGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135	T C ---	---	TGTGAATTCCTAGCTCTGGAAGGTGTTATGCCCTTGGGGTTCTTGATGTGTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGACACATCCCGGTGATAGAAATTCCT /CJAAATTTGCTGAAATAGGTAGAAATTTTCTTAAATTAAGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162	G A ---	---	GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACCTTTGAAGACC AGTCCTGTTTGAGGGAAGCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCTCTCTTGTCTT[G/AJGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162	G A ---	---	GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACCTTTGAAGACC AGTCCTGTTTGAGGGAAGCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCTCTCTTGTCTT[G/AJGGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/CJCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGGAAGTAAAAAATGAAGTCTGACTAGAAATTCATTCGAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTCAG

WI-7555b	60 T C ---			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGT/CJCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGTCATCTCTGTTAAAGCCACTTGGGTG ATAAGAGGGAAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAAGTACATTTAGT ATGGCATTTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTACAG
WI-7555	60 T C ---			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGT/CJCTTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGTCATCTCTGTTAAAGCCACTTGGGTG ATAAGAGGGAAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAAGTACATTTAGT ATGGCATTTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTACAG
WI-7567b	290 G T ---			TGAGCCATCACTAGAAAGAAAGCCCATTTTCAACTGCTTTTGAACCTGGCTGGGCTTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAGGGCGCTACTCTTCAGGGTCTAAAGATCAAGTGGGCTTGG ATCGCTAAGCTGGCTGTTTGTATGCTATTTATGCAAGTTAGGGTCTATGTATTAGGATGCGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGCTCTGTTT AATGATCCCCCTTCGGTCCAAACAACAGGAACCTGACTGGGCAGTGAAGGAAGGATGGCAT/CJ AGCGTTATGTGTAAAAACAAGTATCTGTATGACAAACCCGGGATCGTTTGCAAGTAACTGAATCCAT TGGACATTTGTGAAGGCTTAAATGAGTTTAGATGGGAATAGCGTTGTTATCGCCTTGGGTTTAAAT ATTTGATGAGTTCCACTTGTATCATGCGCTACCCGAGGAGAAGAGGAGTTTG
WI-7569b	63 T C ---			GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574c	216 A G ---			GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216 A G ---			GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCCCTGTTTGTGTTGCCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCCAGGGC/A/GTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216 A G ---			AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAAATTTTGAAGGCGGTACTAGTTACAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCCTTATTCTACATTTCAACCTAC TTTGTAAAGTGAGAGAGACAGAAGCAAGCAANNNNNNNNNNAAGAAAAATAAAC
WI-7576c	168 A T ---			

WI-7576b	168 A T ---	---	---	AATGATGATGATAATGATGATGACGACGACAAACGATGCTTGTAACAAGAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAATTTTGAAAGGCGGTACTAGTTCAGACACTTTGGAAAGTTTGTT TCTGTTTGTAAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTACCTAC TTTGTAACTGAGAGAGACAAGAACAAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---	---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCA[T/C]CAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAITTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---	---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAAGTTCAITTTTGGTTTACACG[T/A]TAGGAAAGAAGAGAGCATCAAAGTGGAGATATGTTAACT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---	---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTCTT TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAITTTTGGTTTACACGTAGGAAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---	---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTCTTAA AAATATGCATCAAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAITTTTGGTTTACACGTAGGAAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---	---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTCTTAA AAATATGCATCAAAATC[G/A]TCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAITTTTGGTTTACACGTAGGAAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---	---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAITTTTGGTTTACACGTAGGAAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---	---	---	AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCTTCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAAGTTCAITTTTGGTTT[A/C]A/CAGTAGGAAAGAAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCAIT/CJCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577b	117	A G ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577	107	G A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCATTTCTCTGAG/GJGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7619g	106	C G ---				ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGTCTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTAAATTAC ATGGCAGGAAGATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150	T C ---				ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGTCTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTAAATTACATGG CAGGAAGATGGGCCCT/CJTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCATCTTTTCCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228	A G ---				ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGTCTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTAAATTACATGG CAGGAAGATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCATCTTTTCCCTCTC CGCTTTCTTCTTACACAGAAACAT/GJACATACCGAGAAACCTATTTC
WI-7619n	237	G C ---				ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGTCTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTAAATTACATGG CAGGAAGATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCATCTTTTCCCTCTC CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99	C T ---				ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGTCTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTAAATTACATGG TGGCAGGAAGATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCATCTTTTCCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A ---				ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAAGGCCAATGGGTCTATCCCTCCCTAACGAGACTCTGCTGCTGGGGTGTAAATTACATGG CAGGAAGATGGGCCCTTAAGGGAGTGTGGGTCTGCTCTCCCTTTTCCATCTTTTCCCTCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---	---	ACAGGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTCTGGGGTGGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGGGGTGGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCTCTCT CGCT/GTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGGGGTGGCTAATTACATGG ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGGGGTGGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGGGGTGGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAACAT/GC/CACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGGGGTGGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGGGGTGGCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTCTGGGGTGGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	ACAAGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAAATGGGTATCC[C]/GJCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAAATTAC ATGGCAGGAAGAATGGGCCCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTTCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTTCCTCTCT CGCT[G]/TCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAAGCGGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTTCCTCTCT TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGC[A]/GJTTAAACCAATCATGACCAAAATGTG CCATACTAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626c	155 C T ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGACCAAAATGTGCCA TACTAATGATGAGCATTTAG[C]/TJACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626b	28 T A ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAGCAACAGTAA TACTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGACCAAAATGTG CCATACTAATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7626	144 T C ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAAATATATGTATTTAAAACAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGACCAAAATGTGCCA TACTAATGAT[C]/JGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTATAGTAACCAATTTCTTTGGACTGTTCA
WI-7689c	134 A G ---	---	TCCCAATACCGCTGATTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTCTAGGACGCCACCCAGCAAAAGGTGTTCTCTAAA[A] [G]TAAAGGCGAGAGTCACACTGGGGCAGCTGTATACAAATTTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGGTGGCGCCACAAATAAATGGAATTTATTAGAAATTCATATGAC

WI-7689b	134	A G ---			---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCGGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---			---	TCCATAACCGCTGATTCTCAGGGTCTCTGCTGCGGCCCCACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAJA AATAAGGCAGAGTCACACTGGGGCAGCTGATACAAAATTCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---			---	TGGAGAACATTCAATCTTCCCGTCACTATTCAATCAATGAAGATTAG/CACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCAACAGCATGGTAGTGGCAAAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTCCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACGTCTCAGTTCAATCC
WI-7703b	164	T C ---			---	ACAGAAAAGTTGAATTTTACATGGCTGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAAACAAGTCAGTCATTGATATGATCAAA TGCTATAAACCAAACTGATGAAGTAAAT/CJGGTCTCTCAGTTGTTTATTTAACCTCTAAATTC TTCAATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156	T C ---			---	ACAGAAAAGTTGAATTTTACATGGCTGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAAACAAGTCAGTCATTGATATGATCAAA TGCTATAAACCAAACTGATGAAGTAAAT/CJAAAGTAAATGGTCTCTCAGTTGTTTATTTAACCTCTAAATTC TTCAATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---			---	TTAAATGAGTGTGTTTGTACCCGTTGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJAGCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAAGCTCTCAGCC
WI-7743d	275	C T ---			---	TTAAATGAGTGTGTTTGTACCCGTTGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJAGCAGGAGTCCCTGGTAATAAGTACT TACAGAAATCTGCTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAAGCTCTCAGCCAACG
WI-7743e	106	C A ---			---	TTAAATGAGTGTGTTTGTACCCGTTGGGATTGGGGAAGACTGTGGCTGTGGCACTTGGAGCCAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/CJAGCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAAGCTCTCAGCC

WI-7743d	275 C T ---			TTAAATGAGTGTGTTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106 C A ---			TTAAATGAGTGTGTTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743d	275 C T ---			TTAAATGAGTGTGTTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743c	106 C A ---			TTAAATGAGTGTGTTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275 C T ---			TTAAATGAGTGTGTTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	106 C A ---			TTAAATGAGTGTGTTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAG GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275 C T ---			TTAAATGAGTGTGTTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7758	144 A G ---			TGACATTTATTCAAAGTTAAAGCAAACACTTACAGAAATTAAGAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC(A/G)TAGTTAACTGCATTATAATTTTATAACAGAAATTAAGTATGATTTTAAAA GATAAAATGTGTAATTTTGTATATTTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C ---	---	ACAGGGCCTTTGGCAGGTGCAGCCCCACTGCCTTTGACCTGCCTCCCTTCATGCATGGAATTCCTT TCATCTGGAACCATCAAAACACCCTCACACTGGACTTGCAAAAGGGTCAGTATGG[G/C]TAGG GAAACATTCATCCTTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTG ACTCAAACCAAATCACTGAACCTTTGCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237	C G ---	---	TTAATTTACTGATTCAGCAAGACCAATCATTTATCAGATTAATTTTAAAGTTTATCCGTAAGTTT GATAAAGATTTTCTATCTTGGTTCTGCAGAGAACCTAATAAGTGTACTTTTGCCATTAAAGCA GACTAGGTTGATGCTTTTACCCCTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTGACGTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C ---	---	TGCAACCTCTTTTCGTGATGGCAGCCTGCTGTGTCAGCACTCCAGTAGCGAGACGGCACCCAGAAT CAGATCCCAGCTTCGGCATTTGATCAGACCAACAGTGTCTTTCCGGGGAGGAAACACTTTTAA TTACCCCTTTTGAGGCACCACTTAAATCTGTTT/CJATACCTTGCTTATTAAATGAGCGACTTAAA ATGATTGAAAATAATGCTGTCTTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAATAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGTAATCCAATTATTATTCACATTTACCA TAATTTATTTTGCCATTGATGATTTATTTGTAAATGATCTTGGTCTGC
WI-7785b	165	G ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAATAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGTAATCCAATTATTATTCACATTTACCA TAATTTATTTTGCCATTGATGATTTATTTGTAAATGATCTTGGTCTGC
WI-7785	156	T ---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAATAAACTGTCTCCCCATTGCTCTATGAAACTGC ACATTGGTCATTGTAATANN- /TJNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCATAATTTATTTTGTCCTTGA TGATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84	G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAAGTGGGGCTGTCTCAGACGACTAGCCAGGACCATCT
WI-7789b	84	G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAAGTGGGGCTGTCTCAGACGACTAGCCAGGACCATCT

WI-7789	73	G A ---			TCTCCCTCATCCAACTCGAAAGTCTGAATCTCCCAAGGAGGGACCACCATCTTACAGAGACTCTCCC TGACG[G/A]TGGAAATTAAGTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190	C T ---			AATTGTCAGTCACTTCTCAAAACCTTACAGTCTCTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGACTAGGCTTGCCATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/T]TCTATACITTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
WI-7790	190	C T ---			AATTGTCAGTCACTTCTCAAAACCTTACAGTCTCTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGACTAGGCTTGCCATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[G/T]TCTATACITTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
WI-7795b	81	C A ---			CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAAATTAATGATTAATAAGCATGCCCTTCTCTCTCTCTCT TAATAAGCCCCACATAAATGTACTTTTCTCCAGAAAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATTCTG
WI-7795	81	C A ---			CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[C/A]GTCATCATCAAGAAATTAATGATTAATAAGCATGCCCTTCTCTCTCTCTCT TAATAAGCCCCACATAAATGTACTTTTCTCCAGAAAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATTCTG
WI-7814c	41	G A ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCC[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA
WI-7814b	41	G A ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCC[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA
WI-7814	28	G A ---			TTCTCTCATTTTATCCCTCACCTGT[G/A]CATGCCAGTCCGTTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAGAAATAACAGAA

WI-7830d	150 C T ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTCATTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTGTTGTTTGTGTCGACATTTTACTTTTTTGGCGTGGA
WI-7830c	54 G A ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTGTTGTTTGTGTCGACATTTTACTTTTTTGGCGTGGA
WI-7830b	134 G A ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTGTTGTTTGTGTCGACATTTTACTTTTTTGGCGTGGA
WI-7830	44 A G ---				GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTGTTGTTTGTGTCGACATTTTACTTTTTTGGCGTGGA
WI-7865e	25 C T ---				CCACTTCCTATCTGATTTTCCAGIC/TJAAATGAGCGAGGCAATCTAGTCTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191 C T ---				CCACTTCCTATCTGATTTTCCAGCAAAATGAGGCGAGGCAATCTAGTCTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25 C T ---				CCACTTCCTATCTGATTTTCCAGC/TJAAATGAGCGAGGCAATCTAGTCTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191 C T ---				CCACTTCCTATCTGATTTTCCAGCAAAATGAGGCGAGGCAATCTAGTCTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA

WI-7865	25 C T ---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGCGGCAATTCCTAGTCTCCACAAAACATCTAGGCCATCTAAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGGTATGCTACTCATAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGCGGCAATTCCTAGTCTCCACAAAACATCTAGGCCATCTAAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGGTATGCTACTCATAGATTTTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAACCTGAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	TTCAACACCTGTCTTCCACCTCCACCACCTGTGCAATCACTTCCCTTCAGCCTCAGCTAGTCCCTCTAACCAATTACCCTGTCAAGAGG[C/G]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATATGGCCTGTGAGTTTAAATGTTTAAATGTTGATTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGTTCTATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ---	---	TTCAACACCTGTCTTCCACCTCCACCACCTGTGCAATCACTTCCCTTCAGCCTCAGCTAGTCCCTCTAACCAATTACCCTGTCAAGAGG[C/G]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATATGGCCTGTGAGTTTAAATGTTTAAATGTTGATTCTTTCTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGTTCTATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTTCAACCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAATCATTTAATATTTCCCTGTCTTACCCTATTCAAGCAA[C/T]TAGAGGCCAGAAAATGGGCAAAATTATCACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTTCAATGCCTAGAT
WI-7868b	173 C T ---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTTCAACCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAATCATTTAATATTTCCCTGTCTTACCCTATTCAAGCAA[C/T]TAGAGGCCAGAAAATGGGCAAAATTATCACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTTCAATGCCTAGAT
WI-7868	66 T C ---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT[C/T]CACCCCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAATCATTTTAAATATTTCCCTGTCTTACCCTATTCAAGCAAATAGAGGCCAGAAAATGGGCAAAATTATCACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTTCAATGCCTAGAT
WI-7870b	85 T C ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTATTAGAAGGGGTGGGGTGGCGGGAATCC[C/T]ATTATCAGACTCTGTAAATGAATATAAATGTTTACTCAGAGGAGCTGCAAAATGCCTGCAAAATGAAATCCCAATGAGCACTAGAAATTTTAAACATCATCTACTGCCATCTTTATCATGAAGCACATCAATACAAGCTGTAGACCACCTAATATCAATTG

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGGTGG[C/T]GGGAATCCTATTATCAGACTCTGTAATTGAATATAATGTTTACTCAGAGGAG CTGCAAAATTGCTGCAAAAATGAAATCCAATGAGCACATAGAAATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGGTCATGCCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCCGTGAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCTCCAAGGCTGCTTCTCCCAGAGCACAAAG
WI-7889b	54 C ---	---	---	TTAGGTCATGCCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCCGTGAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCTCCAAGGCTGCTTCTCCCAGAGCACAAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCCAAATATACTGTTATCCAGAAAGCTGTATGCTCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTGTGAATTTATATTGCGTATAC ATTATC[A/G]TATGTAAATTTGCATTTTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTTAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCCAAATATACTGTTATCCAGAAAGCTGTATGCTCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTGTGAATTTATATTGCGTATAC ATTATC[A/G]TATGTAAATTTGCATTTTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTTAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAAA TATGATGTTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAAA TATGATGTTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACAGTGATTAAAGTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAAA TATGATGTTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC

WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTGAACCCAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T ---	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTTGCGGGTCGCTGGGTATTTGGGCGAGCGCCGTGGTCGT CACACAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33 C T ---	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTTGCGGGTCGCTGGGTATTTGGGCGAGCGCCGTGGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT

WI-7901	33 C T	---	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTTAAACAG ATTGTTTCATCATTCATCTATTTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTGGTTGCGGGTCGCTGGTTATTGGGCGAGCGCGGTGGTCTGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTTAAACAGATT GTTTCATCATTCATCTATTTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCT TTTTAAACAAACTCCAGGCCCTGGTTGCGGGTCGCTGGTTATTGGGCGAGCGCGGTGGTCTGCAC TCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150 C A	---	---	---	CATTCGGCATCTGTCACCGAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACTTA[C/A]ATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	---	CATTCGGCATCTGTCACCGAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAAGATGATGCAC ACTTTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTC ATTTACAATGCAATACTTACATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7926	150 C A	---	---	---	CATTCGGCATCTGTCACCGAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAAGCAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCATT TACAATGCAATACTTA[C/A]ATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTCTGCAATATTTGCAACCTATATCAGAGAAATTACACTGTGGGAA
WI-7947b	203 G T	---	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAAGCAGCCAGACCCACAAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACCAGCCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTTCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGCAGCCAGTGCTGCCACCTG
WI-7947	203 G T	---	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACACCATAAGCAGCCAGACCCACAAAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACCAGCCGAGGCCACAGAAATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTGTCTCAATTCAAATCCATAGATTTTCGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGCAGCCAGTGCTGCCACCTG
WI-7963b	145 T C	---	---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTAAAAATAAAAAATGCC ACAAATTCATTTCTCCTTCTAAGTATTACAATGGAGTTTATCTCTGCCTAAAAAGTGGGAAGAAAT TGAGTGAATGA[T/C]AATTTTGTAATTTAGGATAAGATCCAAGTATTTTCCCAACTCTTGTCTTCCC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAGGCGCAGAAAGCGGAAAA

[illegible]

WI-8021b	57	C T	---	---	ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAAC/C/TGATCCC ACGCTTTAGAACCTTCAACCAAGGAGTTTTCTTGTAGTGATCTCAAGTCTTGGTAGGCATTCTGA ACTGGTCCCTTTCACTTTGAGATCTTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCTTGTAGGGGTGATTGGAATCGGTGAATTGCCA
WI-8021	57	C T	---	---	ACAACTCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAAC/C/TGATCCC ACGCTTTAGAACCTTCAACCAAGGAGTTTTCTTGTAGTGATCTCAAGTCTTGGTAGGCATTCTGA ACTGGTCCCTTTCACTTTGAGATCTTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTTACGTTGCGGCTTGTAGGGGTGATTGGAATCGGTGAATTGCCA
WI-8024c	206	A G	---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTTAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCTATCAACAAACACCATTTAGCCGCTCTAGCCTCTAA TTCCC/A/GCTCTAGAACAGCTGGCCCTGGTGTGCTAGTACACAAAGGAAGAGC
WI-8024b	206	A G	---	---	CTGAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTTAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCTATCAACAAACACCATTTAGCCGCTCTAGCCTCTAA TTCCC/A/GCTCTAGAACAGCTGGCCCTGGTGTGCTAGTACACAAAGGAAGAGC
WI-8077	167	A G	---	---	GAATGAGCCTTCTAGCGCCGAGGGACCTGCTGCTGTGTTGGCTGCACATGCATCTATGGAATGC TTTTTGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNATCGCCCAACTCCTTTCT AAGGAGTCTGGGTGTCATGCCCTACAAACCI/A/GTAAATCTCATCAGATGGATTTATTTAAACGTT GTGTATTGTGACTTACTTTCCAATCTGACTCTGGCATAACAAGGGAATAA
WI-8118f	114	G C	---	---	TCTAGGTTTAAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGTAAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAATACAGAATGAGCTTGTG/GC/TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	---	---	TCTAGGTTTAAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGTAAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAATACAGAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	---	---	TCTAGGTTTAAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGTAAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAATACAGAATGAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44	C T	---	---	---	<p>TCTAGGTTTAATCAAAGCAATTTCANTTTGGATTTTGGAAATGAC/CACACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAATACAGAAATGAGCTTGTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA</p>
WI-8118b	88	T C	---	---	---	<p>TCTAGGTTTAATCAAAGCAATTTCANTTTGGATTTTGGAAATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC/CJGGCAAAATACAGAAATGAGCTTGTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCCTATTCCTTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA</p>
WI-8171d	299	C T	---	---	---	<p>TTTTCTCCTCCGGGGACCAAGGTACCTTCTGGGCATACAACATGGCAGGCGCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA</p>
WI-8171c	46	A G	---	---	---	<p>TTTTCTCCTCCGGGGACCAAGGTACCTTCTGGGCATACAAC/CJGTGGCAGCAGGCGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCAC</p>
WI-8171a	46	A G	---	---	---	<p>TTTTCTCCTCCGGGGACCAAGGTACCTTCTGGGCATACAAC/CJGTGGCAGCAGGCGCTCGGG AAGAGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCAC</p>
WI-8171b	298	T C	---	---	---	<p>TTTTCTCCTCCGGGGACCAAGGTACCTTCTGGGCATACAACATGGCAGGCGCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA</p>
WI-8314b	85	G C	---	---	---	<p>GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAAATAGAATTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCACT</p>
WI-8314	78	C G	---	---	---	<p>GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAAATAGAATTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCACT</p>

WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTGGTACTTTTCAAGAGCTGCTGTATAGTACTCTGAGAAG TCCCTTAGATAAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTTCTTA TTTGTCTATGGTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTAGAGCAGACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTGGTACTTTTCAAGAGCTGCTGTATAGTACTCTGAGAAG TCCCTTAGATAAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTTCTTA TTTGTCTATGGTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C ---	---	TATGTACTACTTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTTCCCTCCCTGTGCAGCCTTAGA/AJ/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTTCTTCCCGAGCAATGCCACTGCAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---	---	TATGTACTACTTTTCAGTTACCCCGTGCCTCCAGAATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTTCCCTCCCTGTGCAGCCTTAGA/AJ/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTTCTTCCCGAGCAATGCCACTGCAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAAGCGGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCOCCATGATCCAATCACCTNTCACCGGCCCTCTCCAACACGTTGGGG
WI-8378	308	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAAGCGGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAAGGAGAAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCOCCATGATCCAATCACCTNTCACCGGCCCTCTCCAACACGTTGGGG
WI-8426	184	T G ---	---	TTTAGCACATATTTAGCATTAAGCCTCAAACGATACAGCAATATGTTACATTTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACCTCCGACTTGTGCCTAATAGGATTTGACCNNTAA GAGGNTCTTTTGTGTGGGNGGGTGGCTTTCGTTGAACCTCCATTTCTG/TG/GCCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCCGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTCTATCTTAGTCCCAAGTTTATGTTTCAATCCCAATTAACCAATCCATTTGTTATTTTAAAG AAAAACCTTCCCAGTTATGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTATCTTAGTTCCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAAGTTTGTAGTTTCAATCCCAATATATACCAATTCATTGTTATTTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTATCTTAGTTCCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAGA AAAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G	---	---	CAAGGAAAGCTGCAGTCTTCATAAACTTCAAGAGTTACAAAAATACGTTATTTTAAAGCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGTACATTGTCACACACCACATCAACCTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGTAAGAACTTTTATTGTGCACAGT GACATCCATTCGCCAGACTTAATGTTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105	A T	---			CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAATCATTTTTT[ATJNNNNNNNNCCTTGTCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38	T C	---			CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAA[CTJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAAATCATTTTTTNNNNNNNNCCTTGTCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38	T C	---			CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAATCATTTTTTNNNNNNNNCCTTGTCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105	A T	---			CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAATCATTTTTT[ATJNNNNNNNNCCTTGTCTTATTACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAATTTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77	A G	---			AATAACATGTTATGAAACAAGCTGGTTACAAGTAGTAGGATGACTTAATTTTGATAAAAAAAT TAAAAAGCAT[AGJACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGATTTACTTC TGCTCAGTAATTAATAATCTTCCCTTTGTTTTGTCITTTTAAAAACATTAATTTCTGAAAAAATA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101	C T	---			ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAATCCAGTCTGCAGCTCAGTACCTGT[CTJGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCGAGAGGCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAACAAACAAAG
WI-9439a	76	C T	---			ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAAT[CTJCCAGTCTGCAGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCGAGAGGCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAACAAACAAAG
WI-9446b	75	T C	---			GAAGCCTTGATTAAAGGAGGNTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[CTJCCCTCTAAAGNGACACATGCCCCAAATGACCGANGNCATAAGCAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTTGTNNCCCTACTNTTATCACTGTGTCTCTGCTCTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75 T C ---	---	GAAGGCTTGATTAAAGGAGGNTTTATTGATGTAACCTTACCATTCCATAGACTATAAAGANCATTATAAAAAAA[G/C]CCTCTAAAGNACACATGCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTCNCCCTACTNTTATCACTGTGCTCTCTGTCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---	---	ATTAATGTCAAGGTTTCATGTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTTT GAGATAATTATTCTAGATCCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAATCTACATGGAAAAGCCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9497	185 A ---	---	ATTAATGTCAAGGTTTCATGTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTTT GAGATAATTATTCTAGATCCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAATCTACATGGAAAAGCCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAGTTTCTATTCTCATCCATCATACAATAGATTGIGCTAAGGATCATTTTGGAGAATGTG CAGCATTCAGAAGTTGTATCTCATCATGCGACTCAGTCAAGGCAATTTATCTAAAAGTACGTGCACA GACTCAGACAAATTACAACTATTTCAAGCATGATCTATGGTGATTTTCCACACATTTGTA[C/A]AGTG AAAGCTCTTCAGCTTGGAACTTGAACAACTTGCAAGGCGAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAGTTTCTATTCTATTCTCATCATACAATAGATTGTGCTAAG[G/A]ATCATTTTGGAGAAT GTGCAGCATTCAGAAGTTGTATCTCATCATGCGACTCAGTCAAGGCAATTTATCTAAAAGTACGTGCA CAGACTCAGACAAATTACAACTATTTCAAGCATGATCTATGGTGATTTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAACTTGAACAACTTGCAAGGCGAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACAAGTTTTCATACATCACAAAAACCTTCCATTATAACACAGAAAGTGATTATTACCAGAG AAGCATCAGTGATGTATCTGCTTTNCTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCCATG CAATACACCCAAAGAACACTAGAGTCTACACCCAAAGTACAATATGATAAGCAGCCCTCTGCAAGTG GT[C/G]GCTGGATACCCTAAGAACTACTGCGAGCCCATGTTGGTTATGATTTT
WI-9555	97 G A ---	---	CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACAATTTATGATCCTTTTGTAGGTAAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G/A]CTTGAATAATCAATTTCAAGGGACTCTTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATCTCAGATTAAAATACAGGTAAGTATTTCAG GGNTAAATGGTACAAAAAGGCTGTAACTCTTTTNCCTCACATTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAAGACATAACATCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCTTGGGAAAAAATTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCT[A/T]GTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172	A T	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAAATTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTA/TJGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTTC
WI-9647	144	C T	---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGTCTACTATACCTTTTTCATCCCTTTCA ACATCTTTTGTACATTTTAGGIGATGCTCTTTGTAACAGTGTATGCTAGACCTAAAAATCCAAGCT TACAACTC/TJGTCTTTTACCTGATACATTTATCCATTTACTTTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCCTGCTTTTAGTTAATTGTGTT
WI-9676n	114	A G	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATTTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCA/TJGATGTGGCTTTCTCGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTGTTT
WI-9676m	184	G T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATTTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTGTTT
WI-9676l	84	A C	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATTTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTGTTT
WI-9676k	202	C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATTTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTGTTT
WI-9676j	92	C T	---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAGATGAAGAAAAATTTGGCAATCTTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTGTTT
WI-9676i	173	T C	---	---	GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ C/AJATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ C/AJATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGGCTTTCTGCCCCQ CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA/C/AJATTACAACATCATGATCACAIGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTATGTGGTGGGCACATGCTGTATTGCTGCC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA/C/AJATTACAACATCATGATCACAIGC AGCAACATCAACATCTCAAGGAGTCCATTTGTTCAAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAGACTCTGCTTGTACCTTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTATGTGGTGGGCACATGCTGTATTGCTGCC
WI-9756	47 A ---	---	ACTGAAATGTAAATGGCCAAGGCCACCCAGGACCTTAAAAATCATAAGAAGTTAATCTGTGGGAAAA GAGTAACACTACAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCCTTATCAGTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAACACACAGATAATACACTTTTGGAAAG ATTCCACTTAACCACTTGATTCTTCACCTTTTATGATTTAAAACTCTCCGTGG
WI-9758	135 A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATTCATTTCAAGAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/A/GJTAAATAAATCTGTAGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCCAGGCAGCGGGGAAAAATGGATACCTTCATATGTCTGTACCCCACTAAACTTTTG GTTCTCATGCACCATTTTCATTTTGCTTCTCACTCCAAGTACCAGTATTTACCAATTTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTGGAAATTTCTTATTACACACTTTGCTCA AAGAATGTGTGAGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCCTCCCTTTGCCCTCATGCCACTCCCTCAGCTGCACAGAGCGTTTCTCCAGTGTAGTCTCGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAATGCAGTTTC/AJTGATCCCAAGGGA CTCAAAAACCTAGGAATTTGGAGAGAGGACCTGGAATCGGTGTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTGAGGACCAGACATGGAAGTTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC/AJGTGTGTATGTATATATATCTTATTAACTTT AGGATTATATACACACAATAAACGCTGTAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTGTTACTTGATATGCTGTG
WI-9880c	222 G A ---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGTGGGTTGAGTTTTTATGATATCTCTGTTAGACCAATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATTTATATTTATATAAGCACATGAA AATGGAATGAAATAATGA/GA/JTTGACATAGGAAATACCTACATATTTTG

WI-9880b	157	C A	---	GAAC TAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTATAGATCTCTGTAGACCCATAAGGGAGGCTGTA GTTGTTTTCTACATCCTTGGAC[A/J]ATATAAGATCCTCTTTTAAAAATATATATTTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T	---	GAAC TAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCT[Q]CTGTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACITTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTCTGGAGTTATTTTAAAAACAACGCCCGGATATCACAGTTTCINTTTTTGTC[Q]CACC ATTTCCATAACAAAAGAGCTACACAAAATTTNGGGGGGAGANACTCTCTTTGGAGACTGCACACATT TGCAGAGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G	---	TCCCTCAATGACAGATGAACATAAATTTCTCTGGGTAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGACAAAGAAAATGGAA[Q/J]TGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATAATTTATACATAAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
FB25G10	109	A G	---	TCCCTCAATGACAGATGAACATAAATTTCTCTGGGTAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGACAAAGAAAATGGAA[Q/J]TGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATAATTTATACATAAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
IB3071	102	C A	---	ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAAATTA GATGAACCTGAAATTTAAGNTAAATAAATAAATAAAT[Q/A]CAATTTTCAGNAAACAAAATCAAAAC ATTAAGNTCCCTGNNATATCTTAAACCCCTAATGAGATTTCACCTGGNCTCAAGTCAATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAACCCAGTCTAGGGATTCTG
NIB551	161	C T	---	CGTCCTTCTCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATGGGTGTCCTC TACTGAGCTTGGGCCAGGTGTACTTAGGAACCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[Q/J]TGACCACACATACATCGCGCCATTGGTTGATTTAGCCTTT GCAAGCAGCGTAGTGAGAAAACCAAAGCTTGTCC
S72904	51	G T	---	AGCATAGAAAGTGATTTATTTTTAATGGTTTTCAAGTGAAGTTCCTTT[Q/J]AATTTGTGCTGTT ATTCCTGGAAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAAACCACAAGTGTGTAACCTCTCCCTTTCTGTCAATTTGGTGTCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTTTTCAAGTGTCTGTGTA

UTR-00481	115	CT	---	TATTCCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAACACAGAGCTTACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	GCTACTACACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	GCCATCAAAATTTCCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	TGCTGGCTCAGTCTCCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	AAAACAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	AAACCTCACACAGAAAAAGAGGANAAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTCCCTTTAATTGTAAAAGCGGG CATCG
ESTC117	24	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAAGTTCCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	GACAATAACACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	GAAGCCAGTATGTTGTGGCAANAATTGGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAAGTGG
ESTC129	20	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGTGTTATGCTGGGAG
ESTC13	46	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAAATCTTCAGGAAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	---	GGTAAAGTCTAAATTACTGCCCTTAGCAAACNCTATGTGTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	---	CCAGTTTGGCTTCTGTCTCTCANAGTCTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTACAGAGTTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	---	CCCATTTGGTCCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCAATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCATTTTAAATC AAGANACCATTCCTTCCCTAACAAACA
ESTC143	29	---	---	---	---	GTTTACGAAAAGTACTGAAATGCTATTANTAGCTGAATTTGTGATTTTCCTTTTG
ESTC144	26	---	---	---	---	AAATCCATATTTTCTTGACATGAGGTNGCTTTTATAGCAGCATTTTCGG
ESTC146	20	---	---	---	---	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	---	TCCTTGGTTGCTACACAGACACTTAAGTACTGTATCGCTGTNATGCAGCGGCCCTGTGGAGGCCCTCG GGGTGGCTGGGCTGTGTCTGAG
ESTC149	28	---	---	---	---	TCAGTTCATTTATTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGG
ESTC15	28	---	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	---	CCAGGAAACAAAGCACACANACTTATAGAATCTTTGGTTTAAAAATTTATCATAATATCAATATT AACTCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	---	GAAGCTAAGGCCCCCATTTTTTCTTTTAAATACAAATCTACTGGTGCTNAAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCATTTTACA
ESTC156	32	---	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCCTGGCTGCCCTGGGATGGAGCGGGGGCGCCTCA CCACCACTGCAT
ESTC158	35	---	---	---	---	ACCAAGCCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	---	AGCTGGCAAGAGACTTCCCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	---	CAC TGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTATCATACCCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGCTGGTGCAGTGGGGGCTGAGCTGGGNGCAGTGGCGAGTGTCACTGGGCCCGTTTG GGACTGGGTGA
ESTC162	36	---	---	---	---	CTCTTCGTCGGTTTGCAGTTGCTGTTTGTTCAGNTACACAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATCTCCATAGAATATTGGTTTGTAAACANCGAATACAATCCAAATATATAACATTAACAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTCTGGATTAGAGGAAAGGTGCCCGCTGTCTTCCATGACTT
ESTC176	23	---	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAAATTTTNCITTTATTTCTATTAATAATACCTTTTAT TCTCTTTATCCCATAAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTGCCAGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATAATCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCAATTCAGCTTG ATTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	---	TCTATTACAGGGTTATGTCACACCNTGTCAACCTGTCAACCTCAAAACAGATGATACATCAGTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACCTTCCCTTAACCTTATCAGTCTAGTAGCNTTTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGTGCTGCTCCTCCNGCAAAGTCTCCACAAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGCGTATAGTAAAGCTCTGNGGAACTCCAAGAATCTAGAGGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	---	TCCTACTTGGGTAGTTTAGCAAAACATTTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGGACAGACGCGNCGGCGCTGGGTGGCGCCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	---	ACACTTAACAGGTTAAATAATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGGATAANAGCAATACTATTGTTTAAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	---	GGTAACTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	---	CTCCAGAGTCCCTCCTCTCANACCAGGGGCAGGAGGAGTTAGGGAAT
ESTC216	49	---	---	---	---	TGGCAAGAAATTTATTTACACTAACAAATTAATTTAATCACAGGTATNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	---	TTTTGTCAATAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAAACAAGTTTCAT AAACACACCCCA
ESTC219	32	---	---	---	---	GTACACATCTGTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	---	---	---	---	TCATTGAAGAAAAATTATGGGTTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCAGAANGTAGTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAAATACACANAACACACACACACACACACA
ESTC225	20	---	---	---	---	TGCACGTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	---	TTCTACTTTTATTTTCATATCCCACCACNATAACGACTCCTTTAATTTAAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	---	GCTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	---	CAAAAGGGTTAGTCATATTCCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTTCCTCTATTCCTATAAAAAATAAAGGAGCAGAAATCT GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCCGCCCTCAATTCATATTTTATCTTGAGCCGCTTGGTCAGGTTTGAT TCGACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACAATACAAAG CAATTTCCCTCAGA
ESTC33	25	---	---	---	AGCACTTCCAGCTCCTTGACGTTGNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAGGGAACCCACCTGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTAA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAATCAATTATGCTGATGGAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCOOOCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTCGCTGGAGTTTGTCTTTGTAACNCTCTCATCATCGAGGCTATATATTA
ESTC50	56	---	---	---	CTGTCCGTGTGAGCCCTGCCGCTGTCCCATGGGCCAGGAGCCACTGGTGGGANCCGGCAGATG TTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCNCTCTCTGGGCACAGATCCCACCACTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATNGTTCAGACTTCAGGAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTTGGCTAGGCGTGTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACCCANAGGGCCACGGGGGTCGGGGAGACGACACTTTTTCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCCTGAGTTGCANGCAGGATGGAGATTTGGACACT G

ESTC72	37	---	---	---	GGGCTTCCAAATGGGTATTGGGGCCAGGAGGCTGGCNIITGGCGTGACGCCTAAAGAGTGTGACC
ESTC74	49	---	---	---	AACAATTCACAGCTACAGGAAATCTAGAACAAATCAAATATTCATCACNTTGGGTTGAAAAAGTTG
ESTC77	40	---	---	---	GAAGA ATGACTTCTGTCTCCATCGGAACCAAGAGTTTCCCCAGNGAGCCCTTCTCTATCTGCGGTTA
ESTC81	20	---	---	---	GGCTACGACAGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGGTCTGAGATGTNTCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATATACANCCATTATTAGAC TTTCACAAACCT
ESTC85	28	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGGTTGGGGAGGCTACAGCCTGACCACATTCT TTTGC
ESTC89	22	---	---	---	ATTGCAAGGAAGTGGAACTGNTCAAACAGAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTTCTCTCGTCTGGCATTCGTCCTCTCNGGCCAGTGTCTCCACCCAAAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTACGGGCAGGATCC
ESTC95	32	---	---	---	GCACGTTCTTTGTTCTCCTCTTCCAGAAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCTG
DWU-100	127	C	T	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGAAGTGTCTCCA[C/T]GCCAG ATCTTATCAATGATCTTTCACTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATGCGATTTTCACAAAATCAAAGAAGAAAGGCTTAGCTG
DWU-177	77	A	G	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC[A/G]GCCCTATTACAGTAGCCAAACCGATGAAACAAACCCCAAGCTATATATACCA GATGAAAGGATAAACAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTATCCCTACTACACTGTGGAT
DWU-286	213	A	C	---	CAAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCCAATCATGCCAGCTTCTGTGCATATGAATGAGATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[A/C]TGGGAACCAAGCCCTATCTGAGTCTTCGGCTCCCTCC

DWU-252	94 A G ---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCCCTCA/GJTGAGCATGGTACTTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85 C T ---	---	GAACATTCTCTGCAGCACCTTCACTACCAATGAGCATTAGCTACTTTTCAGAATTGAAGGAGAAAA TGCATTATGTGGACTGAA/CJTCGACTTTTCTAAAGCTCTGAACAAGCTTTCTTCTCTTTTGC CAAGACAAGCAAGAACGACATTTTGCAATTAGACAGATGACGGCTGCTGAAACAATGTCAGAAA CTCGATGAATGTGTGATTGAGAAATTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	GAAATGTTAATTGGCAGGTGAAAAGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAGGAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAGAGGTGAATGTTGAGGGCCCTTCACTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAAGTCTGTCTCTTCCCTA/GJGCACTATTTCCTCTGTGC
DWU-1537b	89 A G ---	---	CTCTTAACCTCAGTCCCTCATCTATAAGAATAAGGGATTCAAGTTGTGATCACAATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC/GJTGAGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTCTGTAACACACAGAAATCCAGTAAGCAGCAGACACTGGCTGA
DWU-1537a	52 C T ---	---	CTCTTAACCTCAGTCCCTCATCTATAAGAATAAGGGATTCAAGTTGTGATCA/CJTAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTCTGTAACACACAGAAATCCAGTAAGCAGCAGACACTGGCTGA
ESTD-ADAb	196 C G ---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAATTCAGGGTCACTGTTCCCTGCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCCCTG/GA]GCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGCTTTGTCTC
ESTD-ADAa	184 G A ---	---	TCTCCTGTCACTTCTACTCCATTAGTTCAAGGTCAGTGAAAGAACTGGGCAATTACCAAGTAATTCA TGGACTGCCAACTGCGAAACAAGAGGGCGCAGTGAGCAGGAGTATTATGCTACGCGGTACCTT TTTTATGAGGACCGAACTGAGGC/TCTGAGCTCAGATGATCCTGT
ESTD-ANT1	160 T C ---	---	TGCCTGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATGTTTCTTCGGGCCAAGAAGGTATCTACC/GJATAGTGTCTATTAGGCATTG
EST10398-2b	168 A G ---	---	

-177-

EST10398 2a	147 C T ---	---	TGCCTGGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTATGAAGGGGCCATGGTA AGATGCTGCCACCTCTTACTACTTGATGATGTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTCTTTCTTGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14 G C ---	---	ATATCGTGGCCTTAGCJTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---	---	CTTTATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAGAGCAAAACAACATTTCAAGG ATAATGGGGCAATCACTTCTTTCTTTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---	---	AGTCTCATCTGCGGTGTCAGGTAGATCCCTTTACCGTGAJCCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---	---	CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGGCGCGCCAGGCTCAOCTCTATAGTGGGGTGG TATTCGTCCACAAAAGJTGCACTCGGATCAGCT
ESTD- HRASa	37 C T ---	---	CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGGGCTGAGCGGCTCAOCTCTATAGTGGGG TCGTATTCGTCCACAAAATGCACTCGGATCAGCT
ESTD- NRAMP	81 A G ---	---	GGAGGAGGAGGTGGGAGGGGTCTGCTGCTCCAGGTCCACAGACCAGAGAGGGGCTCAGTG TATCCCCACCCCAAGJTGTTGGCGCTGGGAGATGAAGAGGATGATGCAGGT
ESTD-OTC	18 A G ---	---	GTGACCTTCTCACTTTAAAGJAAACTTTACCGGAGAAGAAATTAATATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAGGAGGATGTAAACA
EST36751 7	36 C T ---	---	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACTCTGATTACCTTTTCTTATTTCAAAATCTCTGTA AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTCAAGTTAAACAG
EST40562	109 A G ---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAATAACAAATAGJTTTTTACCCTTTGAAAAAATAA ATGAAGGATTTGACCTGCTTCCGCTGGAAGAGTATCCGTACCGTCCCTGACGTTTTGAAACAATACA GATGCCCTCCCTGTAGCAGTTTCAGCCTCCTCTACCCCTA
EST18288 3	121 C T ---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGAJCTGGGAGCCAGT GTGGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---	---	GGGAGTGACAGCTAGAGCAACCAAGGGGGGCTCTTACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATTCTGG
ESTD-ALB	180 A G ---	---	AATCCAGCAGCTTTAGGAGGCTGAGGCGGCTATATCACCAGAGGTGAGGATTTGAGACCCAGTCTGA CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGAGGAGATCGCTTGAACCTGGGAGGCGJAGJAGGTTGTGGTGAGCCGA GATGGCACCATTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTTC

EST70523 3	182	G T ---			TTCCGCGCAGCCCCCATCTTGGCAACCCTGGTCCOCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTGGTAACATCCGGCCGGCGCGCTCTTGGACACATAGCTGACCCGTTTCGGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGCCCTTGGAGGGGCCAGCCCTG/JCAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
ESTD- APOA2	101	C T ---			CCAGGTGTTGGCACGTGCCTGTATCCAGCTACTCGGGAGACTGAGGCATGAGAACTCTTTGAAC CGGGAGGGCGGAGGTGCAGTGAGCTGACATCG/C/JGCCACTGCACCTCCAGCCTAGGTGACAGGC AAGACTCC
EST58707 7	112	C T ---			CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAC/JCTAGAAAGATACACGAGAC CGAATGTATCAAAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTGAGGCCAGGTTTATA GCACACTTGTCACTACATTTCTGATTGGTGACTCTTGTGCTAAGAACCTT
EST74167 6	137	C ---			AGACCATGAAGGAGTTGAAGCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGCGGCACGGCTGTCCAAGGAGCTGCAGCGCGCAGCCCGCTGGCGCGGACATGGAGGA CGTGGCGGCGCCTGTGTGAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGACACCGAGGAGC TGCGGGTGGCCTCGCTCCCACTCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132	C ---			CGCTGGTGCAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGACCGAGGAGCTGCGGGTGGC CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGCTCTCGCGATGCCGATGACCTGCAGAAAGCGCC TGGAGTGTACAGGCGCGGCGCGGAGGCGCGGAGCGCGCTCAGCGCCATCGCGGAGCGCTG GGGCCCTGGTGAACAGGCGCGCTGCGGCGCGCCACTGTGGGCTC
ESTD- ARSB	126	A ---			GGAAAGAAATGGAGCCTGTGGGAAGGAGGCGCTCGAGGGGTGGCTTTGGCAAGCCCTTGCTGA AGCAGAAAGGCGGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATGAGCTGCTGCATAATATGACCCAAAC
EST36770 4	144	C ---			TGTAGCCAAAGTCACCTGCATCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCTCCGATAGGCTGGGCTGACCAAAATATACGGGTTTCTGTTTCTTCTGATCAT TCTACAAGTTATACTCTTATTGGAAGGCCCTTAAAGAGGCTTATG
EST26021 1	137	A ---			TAATGTAAGCTCATCCCAAGAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGAAACCTGT CCATAAGTAATTTGTGAAGAGGAGCAAGAGAACATCTCTGACGACTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTCTTCTTTTGAACAAGACAAAGCAAGGCC
ESTD- BA511	29	A/G ---			GGGCAACATAGTGAAACCCCATCTCTACA/JGJAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAAGATGGTGCCACTGCA

ESTD- BCL2	116 A G ---	---	AGCTGGATTAACTCCTCTTCTTCTGGGGCCGTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAAAC[A/G]GGGTACGACAACCGGG AGATAGTGATGAAGTAGATCCATTATAAGCTGTGCGAGAGGGGCTACGAGTGGGATCGGGGAGATGT GGGCGCGCGCCCCGGGGCGCCCCCGCACCGGGCATCTTCTCCTCCCA
ESTD-BCR	69 C T ---	---	CAGTGGCTGAGTGGACGATGACATTGACAAACCCATAGAGCCCGGAGACTCATCATCTGCGCAAGA GA[C/T]CAAGAGGTGAGCTTCTGTTGTCCCGGAAAGGAGGAGCGAGCTAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA
ESTD- BRCA1aa	119 C T ---	---	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA[C/T]TGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACA GAACCAATAAAT
ESTD- BRCA1bb	139 A G ---	---	ACTAAATGAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTAAAG[A/G]AGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAATGAAA
ESTD- BRCA1cc	126 A G ---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTCTGAAAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGA[A/G]AGGA GAGCTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST51212 0	122 A C ---	---	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTCCACAAGCCCCAATTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTGTGCTCCCACTCAATACA[A/C]AAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCT[A/G]ATTGCTCCGGGAAGCACATTCAAT CAA
ESTD-C1R	40 A G ---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCT[A/G]ATTGCTCCGGGAAGCACATTCAAT CAA
ESTD-C6	31 A C ---	---	CCCAGTCAGTTGGGGACAGCCATGCACTG[A/C]GCCTCTGGTAGCCTTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---	---	GTTCGGAATCCTCCTCTGAAAGTGGCCGGGTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGGTTAGGACGCGGGTCTGCGTGCATCTTAAGCTGT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGTCTGCGTGCATCTTAAGCT CTGAGA
EST53018 6	67 A G ---	---	ACAATCCAGGTACACATTCCAGAAAGAGGGGTGGTCAGTAGCCTGGTAGGTCCAGTAATCCA [A/G]GGATTTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T ---	---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCAAACCCATAGGG[C/TTGGATACAAAAG ACAGGAAGGAAGGGGTAGAACCATCAAGAGAGAAATAGGCTGGTGACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCTTTCCCGGCTTCTCTCTCACACAC
ESTD- CB23	136 C ---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTTCCCGCTTCTCTCACACATACAGAGCCCTACCAAGGACACAGACGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTTGCCACCCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAAA
ESTD- CB24	145 A ---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGACCACTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACACAGACACCCGCGAGCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	---	GTTTTCTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCCAGGCGATGGAGATCCACGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGACAGGT[G/C]CTACATGCTCTGTCTTGTCAACAGAGTCTTACCAGCAAGGGTCTCTGTCTGCC ACCATCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCGGTG
ESTD- CB27	125 C T ---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTAGCAATAGGTAACCAATAAAAAAT TGIGTGTGGGCTGTGCTTTCAGGAGTGTCTGGAGTCTGCTCATCACTGAC[C/TT]ATCTTC TGATTAGGGAAGCAGCATCCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCTGTTTCATCTGATGGAGTCTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	---	TTTTCTGTTTACCTTGTTCAGATCTTTCAGAGGAATCCCTATATATGCGAGGTATATGA/TTATGTA TTTTCTTAAACAATAAATTTGAAAGTCCAAAATTACCTTGTATCCATGGACTGCAGAATAAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTTCAATGACAGTAG
ESTD- CYP2D6	61 A G ---	---	---	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGAGAGAACAGGTCAGCCCACTATGC[G]CA GGTTCATCATTTGAAGTGTCTCAGGGTTCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	---	AAAAAAACATTTTAAACACCTTTTCAATCATATACACCAT[A/C]ATTTCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTACTTGCAATCTAAATGTCAACTGATTAATGCAAGTTCAACAG ACAACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	---	CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGCGCCCTACCCCTTGTAGTCCATGGGAAAGGCTCTCTGCGGGCGGTG GGGTTGTGGCTATGTGGTGTCTTGTGTAGA[C/TT]GGGGGCTTTGGTTTTCAGTTGCACATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGGAGGCGCTC

ESTD- D17S33a	75 C T ---	---	CATCCCAAGCCCATCTCTAGCCACTGGCAATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGTC/JACACATCCAGGGGGCCCTACCCCTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCG GTGGGTTGTGTGGCTATGTGGTCTTGTGTAGACGGGGCTTGGTTTTCAGTTGCACATTTGCGT ATTGCAGATTGCTTTGTCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCTGGCCCAACATGGCGAAATCAGATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCCTATCTAATCCAGCTACATCGGGAGGCTGAGCGAGGAATTGCTTGAACCCJA /JGGGAGGCAGAGCTTGCAGTGAGCCCAAGATCACACCACTGCACCTACAGCCTGGGTGACACAGTGGGA GACTCTGTCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAAATACATATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAATAAAGAAATTTAACAGAAATATCATTTGT TTATTCAAACTATTTATCAGCTTATTTTATTGGTAAGCCATACATAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGTCTGATGTTTCCJAGJGGAGCCTTGATGTCATTCGTATCTCCT CAGGTATCCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTATTAATTCAGAGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTTCCC AGAAGTGAACATACCTGCTCTCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGAAAGGATGCTCTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTTCCC AGAAGTGAACATACCTGCTCTCTAGAACCCAGAGTCATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGAAAGGATGCTCTGGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCC[A/G]GCTCTCTACATCATCTTTTCAACAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCTGGGAGAGGAGGAGGAGTGGGGAGGAGACA GAATGCTGATT[A/C]TCTGGTGAGAACCAAGTCTGTCCTGTGGGTAGGGGCAGCTGCTTCCAAAG ACCTCCTGATTGAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGGACACCGAGGGCTCCAGGCTGGGGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCTCCAC[A/C] GJTCCATGGGTGTGGGGCTGGGACCTCACTGTCCTGGGAGAGGAGGAGGAGTGGGGAGGAGAGA CAGAATGCTGATTATCTGTGGAGAACCAAGTCTGTCCTGTGGGTAGGGGCAGCTGCTTCCAAAGA CCTCCTGATTGAGGAAGGGGAGCAGCAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T ---	---	---	TCCCAGCCCTATCGGTCAATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAOCCATCAC ACAAACGGTCAGACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGIC/TTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---	---	---	TCGCTTTTGTGAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCCGCCAAACCCAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---	---	---	AAGAGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCTGGCTGG CACCTGTGAGTCTCTGCCCCACAGGTGTAGTTGAGGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---	---	---	TCCTTCAGGATCCGCATCTCGCCTGTTGGGATCGCTCGCTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGGTGGTGGGTGAGTGC/TGGGGCGGTCAGACCCACGCCGCGGCTGGGAGGACTTCA CCCGCCTCACCTCCGTTTCTGCAGCAGTCTCCGATCGTACT
ESTD- ETS2	43 A G ---	---	---	ACTCACAGTGCTTTTAAGTGAAATGTCGAGAAAGAGGCAC/C/GGGAAGCCGCTCTGGCGCCTG GCAGTCCGTGGGACGGATGTTCTGGCTGTTTGGATTTCTCAAAGGAGCGAGCATGTGTTGGACACA CACAGACTATTTTAGATTTCTTTGGCTTTTGAACCCAGGAACAGCAATGCAAAAACTCTTTGAG AGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTCAGAAAGTTAGTTG
ESTD-F9	111 A G ---	---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTATGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGTATGATGTTA/GJGTCAAACCTCATTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---	---	---	CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCACTCATGACAAATTTGAAGCTGACAAATACACAAGAAAGGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTTGAACATTTGAAGTTGTTTGAACCTGGTGTACCTTTAATTAACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GODH	200 C G ---	---	---	CGCAGACCGGTGAGTGGGGTCGGGAGTGTGAGGGAAGGAGGGAACCTGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGGAGAACACAGAGCCCAACTGGCTAA GTGTAAGGGACCTCTGGTGCACCCGTGTGTTCTGCTGCCCTGTTGAGCTGTCTGTCTGCCGAGT/C G/GACTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	88 A G ---	---	---	GTTTTATGATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA/GJACAGTAAGCCCTGGCAGGAGATCCCCCACCACCCACACCTGGC TGGAGCAGGAAATGCCGAGCGGGCTGAGCCCCAGGAGGAGGAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCCTAATTACTCAAAAGCTGTCCCGAGGTACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGAGAGAGAGGGCCAGGGTATAAAGGGGCCCCACAGACCGGCTC[AT] AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCCCTAGTACCTCCCTAGTGAGCAAGATGTGCTCGATCCAGGGTCAAAACCAC[AG]GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTTACAGTAAGTGCATGGTCCCTAGG
ESTD-HT2	154 G ---	---	GGGCTAAATTTCCGAGCAACTTTCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGTACAGAGAAATAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTTACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACAAAGCCCCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTTGTTTTCTTCTTTCATCTTATAGATTGATGTTATGCTOCTA GCATTCGGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGAGATATTCCTCTACAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCCCCCCTCTTCTCTCTCCCTTGG CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCCAGCAAGAGAAAAGAG[AG]CCCCAGA AATCACAGGTGGCACGTCGGCTACCGCTACCGCACTCTCCCTTCTCACGGGAATTTTCAGGGTAACT ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGTG[C]TCTGGGAGAAAGGAAGATG TTCCAGGGCACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAAATTGGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAATAATGTTGCCTACATTTGTGAGTGACGGGCGAGTGGTGGATCCGAGAGTGTGGTGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGATACGAACTGAAAGT ATGTAATACTTCACAAAATACATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATATTATTATTATTTATTTTGTG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGAGTGCG[AG]CAATCTCGGCTCACTGCAAGCT CTGCCTCCTGGGTTTCATGCCATTCTCTGCTCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTGTAGTATAGACGGAGTTCACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTTCTCTGCTC[AG]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGGTGGTGGACCCAGGCCCCAGCTCTGCAGAGGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGGTGAGCCAGGGGCCCAAGGCAAGGCACTTGGCTTTCAGCTGCTCAGCCCTGCCTGTC[AG] TCCAGATCACTGTCTCTGCAATGGCCCTGTGGATGCGCTCCTGCTGCGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTGTGAACCAACACCTGTGCG

EST45311 0	151 C T ---	---	---	GCCCTCCTCTCTCCAAATCTGTCCCTATAGTTTCTCTATTAAAGTGAACATACATGCATTCTTTAGT GGATAGATGCACACAAACACAGCCATTATGGGAAGGATCCACGCTGTGGCCCATATTGTAACA CATTTTCTGCAAAATC/TACCTCTTTCAATTTAAAGCCCTTATCAATGGCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G ---	---	---	TGCCCCATCAGCGCGGAGACATGGCTTGCACAGCTCTGAGGATGTCACCAATTAACAGAAAT CCAGTTATTTCCJAGJCCCTCAAATGACAGCCATGGCGCGGGTCTCTGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCAGATCTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTCGGTCTCTGTGCAAGTCAGGACATCAGTCTGAATAAA
EST38216 3	26 A T ---	---	---	ATGCAGGATGAAGGTGGACAGGGAGGJATGAGGGCCAACTGTATCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149 G T ---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAA TTTTTTTCTCTG/TAAAGTCCAGTATCCAGAGTTTGGTTTGAAGTGAATGCAATGCCCTGTGAA AAAGAACTGAATACCTAAGATTCTGTCTGGGGTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGTCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT10a	133 A G ---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTA/A GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTCTGTCTTTTAAATAGT TCTGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8b	231 C T ---	---	---	ACCCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGGCCCATAG GCTGCTATCTCTCCCGTCTCAGGTTTACCA/C/TGTCAACATTGACACA
ESTD- KRT8a	21 C T ---	---	---	ACCCTCACCCCTCCCTTAGCC/C/TGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGGCCCAT GGCTGCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T ---	---	---	CACCTGTGTGTGTAGATCTCCTCAGTGGCGCCCTCTACTGGTTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGGCTGGCCCCACC CCTTCTCCTTGGCGCTCTTGAGGTGTGG

ESTD- LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATTTCAAATTTGTAACCGTAGCAAACTGCATTGGTATTTAGA AAAAATAAAAAATTTCCAATATGTAGTCTGTGTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACC/G/GGGAGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACGCGCGGCAATCCTGACACGTTGACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG/A/CACAGATTCCTGGAAGACACAGCAGCGGGATGGGGCAGGAGAAGAGCTGCCTGGATGA A
ESTD- LMP2	35 C G ---	---	TACACACTTTCCTTACCATTCACTGAAACGACTC/G/GJCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACCTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGTTTGTCTTAATCTCAATTCATGTCTCTCATCTTTAG/C/AGCTGTGGGTTTTGTGTTG TTCTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATTATAAAAGAGATGTATCTAAACAAAATAG AGATTGTATCAGAAGTTCACAACATTTATTAAAAATTTTTTCACTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTCTGATGCTGCCTCCCGCTCTGCTAGC/C/AGAACTTCAGGACAACGTGC AG
ESTD- METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAACACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGTCTTTCCAAAGGTTTTGCTCAAGTGTGCTGATTACCC/C/AGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGTTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAAC/TAGTACCAGATCCACAGACTGATATGGCTGGT AACATGGACTTGTATATTTGTACAAAAAAAGTTTTATTTTCTAAAAAAGAAAAAAGAAAA AAATTTAAAGGGTACTTATATCCACACTGCACACTGCCTA/G/GCCCCAAAACGCTTATTGTGGT AGGATCAGCCCTCATTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTGAAATTTCT GAGAAAACCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD- NFKB1	107 A G ---	---	TGTCCTAGGCCCCAGCCCTGCTTGTCTCCTCCCTGGCTGTTATCTC/A/G/GTACTGCAAAGAGAACACA GACAT
ESTD- NPPA	45 A G ---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTCTGCAGGCATATAGAATTTGGT GGGTTTTCTTTATGAGGGTGAATTTGGATACITTTTGTGATTATATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG C/TATCCCTGTGGTTTTTAATAAAAT
ESTD- NPPAS	202 C T ---	---	GCCACCAACCCACCCAGCACACCTCCACCTCAGCCAGACAAGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG/A/G/GTCAGCCGTTATCATCGGAGGCGCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTCTAGACAGACAAAACC
ESTD-PAI1	100 A G ---	---	TAGACAAATCACGTGGCTGGCT

ESTD-PAR	120 A	---	---	CTCTTCAGGAACCAACAGCTCTTACCAAAACAGCATTATTGCTGTCGAGAGGTACAACCCGTAGA ACTTCTTCTAACTGTAAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTCAITAGCTGTGTGAGTGTCTTCTTCTTCTTCTGTTCTTAGAACGTTTCTTAG GACTGGCAGTTTAAGCTTTCACCTTAGCTTCTGTATACCCATGCC
ESTD- Per/RDS	74 A	G	---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTG CTGGAGA[A/G]GAGCGTGCCGGAGACCTGGAAAGGCT
EST68308	5	29 C	T	GGAAAGAGATTTAAGAAGCTTGATTTGGA[C/T]AATTCCTGGTCTTTGAGTGTGAAGAGTTTCATGTC TCTGCCTGAGTTACAACAGAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACITTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045	6	39 A	G	GGAAATATTAAAAATATTTTAAATACCTCCATTTTGCTT[A/G]TCTTTTAGTGAAGATGATACCTGC AAAAACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTTGCCCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD- PXMP1	88 A	G	---	ATGAAACATGGTCTTTAATTTTATGATATGTTTGTATTAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAAGAGGGGAAAA[A/G]GAGCGAGCTGTGGTGACAAAGGTGTTTCTCAAGGCTCATAC AGATTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTATGAAATTTATAATCTT
ESTD-RDS	127 A	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGGTGGCTGTGGAGAAGCGTCCCGGAGACCTGGAAGG CCTTCTGAGAGTGTGAAGAAGCTGGCAAGGCAACAGGTGGAGCGAGCGGGCGCAGACGCGAGG CCAGGCCACAGAGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAAGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- s14544	94 G	T	---	TTGGGAAGTTAGAGCCCTATATTAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAAGTTGAAATGCTCAGTT[C/G]TGTGTGGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	45 A	C	---	ATCACAGTCTGTGTCTCTGGCCATCATTTCTCTGGGAGAGATGG[A/C]TGGTGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55 C	T	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGTAATGACATTGATGAGTGAAGATGTT[C/T]GGCTCAG GATGCCGGAAAAATGAC
EST76136	39 C	T	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCC[C/T]GCGTCATACCTTTATCTATAGCCTT CCCTAGGTCTT
ESTD- SPTB	176 C	T	---	TGAACACCCCTGTGGTCCGGAGCCAGGTTGTGTTCTCTCTGGAGCCGTGAGGAGTTTGTGTGTGTG CAGTCCCCCGCGCCACCTGCTGGTTGAGCCTGGACATACACCTTACCTCTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACA[C/T]CCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCCAAGCCAGTTTCCTAGCAAGGGCAGGAC

ESTD-TAT	224 C ---	---	AAATGGTCAGGACCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTCATTACGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTTCATTTAAATGACTTGTGGGACAGGATCA ATTTCCCTCACTAGAACGTTTGTACAACTTTTCTCCAGATGGATGGGATTATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THRb	125 A C ---	---	TGGGGCTTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCAGAGAAAGAGTCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACAGAGATC(A/C)TTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTCTGTCAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTGTCTCATGGCAAAATCAATGTCCTCCAGATTCA(G/T)ATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYR	122 GT ---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTTAACTGTATTTCTTTTACCTTTATACCTTCTTTCT AATACAAGCATATGTTAG(A/C)ATTAAAGTCTAGGCATACCT
ESTD- TYRP1	222 A C ---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTTAACTGTATTTCTTTTACCTTTATACCTTCTTTCT AATACAAGCATATGTTAG(A/C)ATTAAAGTCTAGGCATACCT
ESTD- VB12	148 C T ---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA(C/T)CAGACTGAGAACCACCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA(C/T)CAGACTGAGAACCACCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACAC(A/G)TGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTACAGAGACAGGAACACCA GTGACTCTGAGATGTCAACCCAGACTGAGAACCACCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607	105 A G ---			CTCTGGATGGGTTACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAGGACAGCCAC[A/G]TGGCGGGGATGGCCGGCGGAGTTC TGGTTGGCGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGGGTTGGGATGCCTAAACCTTTGT TTCTTGGCCAAGGAGGGGGGGTGCCTAGCTGAGATGTAGTGGGGC
ESTD-VWF	36 G ---			AGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770	189 C G ---			AGCACCACTCTCAGCTCAAGCCTCAGCACCATGCTGTCTATAAGGATGACGTGCTGTTTTACAA CATCTCTCCATGAAGAGCACAGAGAGTTATTTATCTGAAGTCOOGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAG[C/G]TGTGGTGGA AGGAGTGCCCAAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAGG
ESTD-TNFab	152 A G ---			TTCTGCATCTGTCTGGAAGTTAGAAAGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTACGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGATCGAGCAGGAGGATGGGGAGTGGGAGTGTGAGGGGTATCCTTGTATG CTTGTGTCCCAACTTCCAAATCCCGCCCCCGCGATGG
ESTD-TNFa	88 A ---			TTCTGCATCTGTCTGGAAGTTAGAAAGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTACGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGATCGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGTATGCTT GTGTGCCCAACTTCCAAATCCCGCCCCCGCGATGG
EST52418	113 A G ---			CAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCCAGTCACCCCTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGAGTTGGCGGAGTACGGGCTGCAGGCATACACT[A/G]AAGTGAAAACCTGTGAGTG TGG
EST13586	89 A G ---			CCCACCTATTGGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGC[A/G]GGGCTGGCTTATCAGCCTCCAGCCACAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCCTGCC CCGGTCACTC
EST51976	123 A T ---			AGGCAGAAACTGGGCCCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTTCTTCAAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[A/T]CTCTC CTCCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGCAGGAGGTCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCGCCCTGGTGC
EST11458	140 A G ---			CCACTTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCCAGTGTCTATCTTCTCGAGTTTT CTCTGCCATGTTGCTATTGACGACGGACCTTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC[A/G]TTAAACATTTCTATGAGCCAGGAGAAGATACGTATTCCTGCAAGCCGGGCTATGTG TCCCAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGC/C/TJAGCA CTGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	CGGCTTCCTCCAGGTATTGTTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCOCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTCTT/C/GJGGTACAGAAAGGAGATGATGAACA GCAGGAACACGTTGAAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCTCTGGGGCCCGTGG TCCTCTGTGCTGTGGGTAGTCTCTGGAGTCAACGGTCTCTT/C/GJGTGAAGCTGGTCTGATGGCA ACCTGGGAACGATGGTCCCGCAGGTGCGATGGTCAACCCGGACACAAGGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	AGTGACTTCCAAGGAATGGTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACCTGCAAGAACAGCATTTGCATACATGGATGAGGAGACTGG/C/JAACCTGAAAA AGGCTGCATTTACAGGGCTTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTTCACCTTAC ACTGTTCTGTAGATGGCTGCTCTAAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	AGAAATATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTTCTCTGCTCTT/C/JGJGGGTGTTCAAGGTGGAAAA GGTGAACAGGGTCCCGTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACA/C/TJGGACTTCTTCTACTGCGAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAAGATATACAATACAATTTTATTTGACCAAAACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGCAATGCCGGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGATGCCTTAGAA GGCAAAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAC TGGGAGGCCCGGCAT/C/JGTGCTCATGCCCTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCCTTACCCAAAGTGAT TACATAAAGAAAGTCAAGTGTTTTACTCCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTG A/GJTAGTAAATGACCGATGGGGTCAGAACTGTTCTGTCAACCATGGAGGATACTATAACTGTGAAGA TAAATCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGCTCTATCTCCAGCGGCCCTGTGATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCCGAGGCACTGGGCTCCGGAGGACTCACCAGTGCCTCCT GCTGCCATGAGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTACATTTGTGGATTGTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAAGTTGCTTTGGCTGCCTGTGCTTGTGGGATATTTGAAAGAGATCTTTTGCCAGTCCAATGTCTCTAGAGATTTCCCAATGTTTCTTGTGTAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATTTGATTTGATTTCTGTA
ESTD-RVRI	109 A G ---	---	CTTCGTACGGGAGGTACGCTCTCCGCCCTCTTTCATGACATATGGATGAGTGTCTGACCATTTCCCTCTGCTGACAGTATGACACGACACTTGTCTACTATGAGTGTGGGGAGCTGTGTGACATCATGCCCGCTCCCTCTGGAGGCTGAGCCACTGAGATCAGTGGAGGCCACCTCGCTGGGGCCAGCCACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTTCACATGTGCTTAAAGCCTCCCTTCCCTTACTCTCTGCTGACGAGTGTGCGTGTGCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2	100 C ---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCACTGTGCATGCACGCTTAACCTCTGCACCAATGGCTCCAAAGCCCGTAGGGGAAGTGGGGGATCTAGGGGATGGGTGAGGAATGGCCAGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGGAGATGGGCTGGATGAG
EST444387	62 C T ---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACCTCAAGGA[C/T]GTCTCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
ESTD-PBDA	103 A G ---	---	CCTTCTCATGCCCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA[AGT]CTCTACCCGAGCTTGCTCGCATACAGACGGACAGTGTGGTGCAACATTGAAAGCCCTCGTACC
EST128393	122 A G ---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAACACACAGCAGCTTACTCCAGAG[AGT]CAAGTCCAAGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTTATTCAAC
ESTD-CTLA-4	48 A G ---	---	TGGATTTCCAGTAGGTTTTCAGTTACTTATGAATATTATGATACCTTAGCTTAGATGGCTTGCCCTTGGAATTCAGCGGCACAAGGCTCAGCTGAACCTGGCT[AG]GCCAGGACCTGGCCCTGCACCTCCTGTTTTCTTCTCTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAAAGCCAC
ESTD-ACE	96 C T ---	---	GATCAAGCAGTGCACACGGGTACGATGGACACAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCAGTACAAGGATCTGCC[C/T]GTCTCCCTGCTGCTGGGGGGCCAAACCCCGGCTCCA
EST544198	88 A G ---	---	TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAAATCGGCCTGCTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGGACCTTTATGGCACAAATGATCACTATTTCTTGACCCCTACTAC[AG]ATCCTGGGAGATGTATTTGGGTTTAGCGTGGTATGTTGTTGCTATATAGTCCAAAGTGAA

-191-

ESTD-PS-1	99 A G ---	---	---	GGGAGTAAACTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACACCATAGCCTAGJTTCGTAGCCATATTAATGGTTTGTGCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATGGCAGCTCTTCCATCTCCATCACCTTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	---	GGCTGCCAGGGTTCCGTGGAGGCGGCCCTAGCGGGGCCCTGCTGGCGCTGGGGTGGTGGCCACC GTGGGAGGCAACCTGCTGGTCACTGCTGGCCATCGCCCTGAGACTCCGAGACTCCAGACCATGACCAA CGTGTTCGTGACTTCGCTGGCCGCGAGCCGACCTGGTGATGGACTCTCTGGTGGTGGCGCGCGGCCA CCTGGGCGC
WI-567b	48 A G ---	---	---	TCTACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTGGTTCAGJAGCCCTCATCTCTTTTA CAGGATCCGCGACAGCATCCCAACTGATCTGGCCTTAGGCTCTCTTCCCAATCCATCTTCAAAAG GCTGCCACTGTGATCTTCCCAAAGGTGATCTGATGCTACCATCTTGCITCAAGCC
WI-801c	58 G T ---	---	---	ATGGAACATTTCTCCATAATGAATGAGTTCTCAATCCATTACACATCCCTTTCTGJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGATTAA CATTTCTGCCACCCCTC
WI-801b	58 G T ---	---	---	ATGGAACATTTCTCCATAATGAATGAGTTCTCAATCCATTACACATCCCTTTCTGJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCAACAGAGATTAA CATTTCTGCCACCCCTC
WI-1099b	76 A G ---	---	---	GAAATTCACTATACAAGAACTATTTCTCTAATTAATTTACATTAGTCTCATTTCTGAAATATTAT TTTTTACAAGJTACCCCTTTGATTATTTTGTATTCTTTGTAAACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATGCTATCACAAATGTCTAAATACCTTTTGGGTCAACATCAAAATTAGAAAAGAAA CTTACAAAGTTTATTGCTTTATGGTTA
WI-2529	71 C T ---	---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCAATTAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA[C/T]TCTTAAGTCTGCTGCTTCACTGAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAAAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	---	TAAGGGCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACATATAAGAGAGACCTGTACCTTATGAGGTAACCTGAGGATGAAGGA GTGAGTCATATTGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTTACATTTTAGAC AGG[C/G]AGCAGAGCAGCAAGGAGAAAGGAAGT

WI-2625	98 G A ---	---	---	GGG CAG T C C T G G C T G A G T A G A C A G C A C T G A A G G A T G G A G A G A G A G A A A C A G C A G A A G C A C T G C A G G A G C T T A T T A G G A [G/A] C A A A T T G A T G A T A C C C T G A G A C T G C A G A A T T A C C A G C A G G G T T A T C T G T G G T G A A T T C A G T T A T C C A C T T G C A G G A A G C C A G C C A G C A A A G
WI-2924	54 G A TAGG	---	---	T C T G T T G C A T A T T C C C T C T T G A C T C T G A C C T C C T A G C T T A T C T C T T A T A G G [G/A] A C C C T G T G A T T A C A C T T A G G C C T A C C T G G A T T A T T A G A C A A T C
WI-2939	72 G T G T G C C T T T	---	---	C C A T T G T G A G G T T G G G T G G G T C A C T T G T C A T C C C T G C A C T A C A C A A G T G G C T T G T C A G T G C C T T [G/T] C A A G A C C T C C C T C A C A A G A A T G T C T T T C C A T G C T C C G T G T C T T T G A A A A T T G A C T T A T C C T G A A A A C T C A G C T G C A G T G T A T C C G G T A T A A G C C A C T C C T G
WI-3203	99 G A A G C G A G	---	---	C T T G C T A C C A T G C A T T C A C A G C A T A C A C C C T C A G T G A A T G C C G T A A C C C C C A T T A T A A A C A T C T T G C C A T C G A A G G G T T A T G C C G C A G A C G A G [G/A] C C A C A C A A G G C A T A C T T G A A G T G A C T T G G A G A A T A A G A T T T G G A T G G A T G A A G C A G A A G A G A T G C T A A A A G T G A
WI-3473	101 A G G C C T A G G G A	---	---	G G A A A A G A A A C C T G A A G G A T G A T A G A A G T T A A T T G G G A G A T A G T T G G T A T A G C C C T G T T T G G A G A T T G C A G A A G A A G C A T T T A G C C T A G G G A [G/T] A G A A A T G T T G T G A C A T C A G G G C T A C A C A C T T T C T G T A T G C T C T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G C A T T G C T T G G C T C C C C
WI-1796b	29 A G ---	---	---	A C A C A C T T T C T G T A T G C T C T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G C A T T G C T T G G C T C C C C
WI-1796	29 A G ---	---	---	A G T C G T C C A T C T T C A G G G T C T A A C T C T G A T C T G G C C T G C A G A T A G G A A A A G A T G G G T G A G T A G T C A C A T T A G G T A T T T C C A A A T A A [C/T] A A A A T G C C T C T G A A A A A T A T C T C T C C C A T G T C C C T G T C T A A A T A A C A T T T T C C C
WI-4360	93 C T A A A T A A	---	---	G C T G A G C T T T G T G G C A G A G C C A G G G A C A A T T C A G C T G C C G G A T T T T A A T A G A T T C T G C A G C A C T G C A A C A G A C C A A A A A T C A G T C [C/T] G G G T A A C T G A G A G T G G T T T C A C A C C C A A A
WI-1959b	87 C T ---	---	---	G T T G T G C C T G T A G C A G A C A C A G A A G G C A [A/G] A G A G G A A A A A G C C T T T T T G T C C A G G G C T T A C A C T G A A T C C C T C A A A C A A T G C A A G A T G A G C T A A T G G T C T T A G A G G T A T A A T C T A A G T G T G A G A A A A C A A A G G T A T A G G G T T T G
WI-1973b	28 A G ---	---	---	C T T G A G T A G C G T G G A T T T G G T A T A C A C A G A A A T G G G A G A G C T G G A A C T A A T C C C C C C A T A T A C C A A G G A C A A A T T G T A T C T G T T C A C A A T T A T A C A G T A G G A G A C A T T A T G T C C A T G A C A A T G G T A A T T T T A A [C/T] G A C A G T T T T A A T T A G T G A A A T T A C C A T A A A A A T A A T A A T A G T A G C A G C T A A T A T T A C T G A G C T G T T A C T A G G T G C C T A T A A A T A G C
WI-1980b	140 C T ---	---	---	

WI-2015b	190 A G ---	---	TGTCAGATAGTCGGTCTCTACCTAGGTGCGAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAAATACAAATTACTTGCAGATAGCATGACCATGCTAGTAGTAACCCACAGACTAT GTGTGAATCGTCTATTAGGGTTTGTCTATAAACTCTACATGGTGCTTTTCCAACTA/GJ/CATATACTT CTAATACCATAGAG
WI-754b	49 C T ---	---	GAAGGCACAGGAGAGATGGCTGTCATCTACAGCCAGGAGAGAGAGC/GJ/TACATTTATTGGTAA TCCTATAAAGTGCACTCTTTAAATTTGTATTACTTTAGA
WI-754	22 T C ---	---	GAAGGCACAGGAGAGATGGC/GJ/TGTCATCTACCAAGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCACTCTTTAAATTTGTATTACTTTAGA
WIR-1b	56 A G ---	---	AGGCAATCAGACCTACAGAAAGGAACCCCAATAAAACTCTGATGATCGTACATCC/GJ/TGCGCTG GAGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTTGAGCCCTCCCTG
WIR-1	56 A G ---	---	AGGCAATCAGACCTACAGAAAGGAACCCCAATAAAACTCTGATGATCGTACATCC/GJ/TGCGCTG GAGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTTGAGCCCTCCCTG
WIR-3b	72 A G ---	---	TAAATTTAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT/GJ/TCTAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGACTGATAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---	---	TAAATTTAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA/TGTATCTAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGACTGATAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---	---	GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---	---	CGGCACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---	---	CGGCACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---	---	CGGCACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5c	177 C	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAAACACAGG TTTACGTCCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-5a	37 A	G	---	TAACCCCTGAAACTTTGTCTTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGCTTGGGGTGGGCAG
WIR-6	63 A	C	---	TTCTGACTATTTC/AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C	T	---	GGCGTCTCTATGACTATCTGTGCTATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-8	46 C	T	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAGTTGTCAGAAGAGGTATGA[C/G]CTGAAG AAAGAACTACTCTCTTTTGACCAATAAATACAAATGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WIR-2	56 C	G	---	TGTCCTTGCTTATGCCTGCCTCTTTCGCTTGGCAGGATGCTGCTCATTAGTATTTCACAAGAAAGTA GCTTCAGAGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCCCTTTTCAGAGTTGGACTTCTAGACTCACCTGTCTCAGTCTC
WI-7069	93 G	A	---	GGTCATTTCTTTTATCTGTCTCAGGCAGCCAGCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A	T	---	CACACTGTTACACACCTATATTTCAAGTTTGAAATGC[A/G]ATTTTGAAGCAGCAATACAAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAATTTATGAAAACATCCCT
WI-18612	37 A	G	TGC	TTGTATTGCTG CTTGCAAT

WI-18517	87	C T	CAGGAATCAG CAGCCTGA	TGTTTGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]TTGTCACCTTGTCACCAACACAACTGACTGC
WI-18668	76	C T	GGCGAAAAAC TAGGCAAAA	GCTAAATTAAA CTGCACCTTTT GC	CGATTGACAAACCTTTTATTTTCAACTTAGGTAAACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAA[C/T]AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTCCCTCTACT
WI-18680	75	T C A	GCTGTCACTCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[C/G]CTCCGTTGTATATTCAAGAGGGGA
WI-18704	99	A C	GGTTCCTCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTTTGCGAGACCAACACCAAGGCGAGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCGAGGGGTAC[A/C]CCAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	TGTGGCAAAACCTTGTATTTAATTGCAAA[C/G]ACTTAATTTACAGCACATTCAATAATGAACCAAC AGGAGATTGCTGACTTTGTAAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GTCGTGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTTATTGGAGGTTAATTCCTATTAGGATATGAAAGGATTCAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAAGGTGCTGGGTGGGGGTGCAGAG[T/C]GTGTCCTCTTC AGTGGTATTGCGGACC
WI-18533b	91	T C	---	---	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTTCATCCTAA[T/C]TTACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	---	---	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTT[G]CTTTA TTTTATATTTTCATTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TCATCTGATAC CTTGTTCAGAT TTC	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTTCATCTGATA CCTTGTTTCAGATTT[C/A]AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGTCTTTCATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAAT[T/A]TGCCCTGGCCTGAAAGTGGCCCATCATACCCCACTGTT CT
EST10030 7	98	T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTTCATAGAGGAGACCTAGGAGGAGTTGACACAGACACTGCTCAGCAGATGACTTAAAAATTT CCCTTAGCCATTTTGTCTCTCAAGTCCCCT[T/C]TCATCCATACCACCACCTGCTGATTTC
EST10052 2	24	G A	GCTCACTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[G/A]GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCATAACCTGGTGGGAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

EST10605 2	118 C G ---			CTCTCAAGTAG ATAAGAGGCA TAATCT	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	CTCTCAAGTAG ATAAGAGGCA TAATCT	CCTGCGTAATCACAGTTCTGTATTATACAAAAAATTTGTTTCTCTGACAAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCCATGTC/GJTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G			ATAAGAGGCA TAATCT	ATAAGAGGCA TAATCT	TTGTTT	ATAAGAGGCA TAATCT	CATGTGTCATCCCATGATTGAAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA ACAAATTTCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAAAACCCAGAGAGGAGCAC
EST11260 8	101 G T					---		TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGTGAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG/GJTGGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T					---		TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCACCACTAGATTCTTTGGACGAAGAAAAATCCT TCTGTGGATTACGCTTACCGCTTTCCCTCATCTGCTGGTGTC/JTTCCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G			CCAACCTACTT TGGAGCCCT	CCAACCTACTT TGGAGCCCT	T	CCAACCTACTT TGGAGCCCT	GAATTCGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAAGAGCATCCAACTACTTTGGAG CCCT/JAGJAGGAGTTTTAGAGAAAGCTGGAGCCGAAACACAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGGA
EST11772 6	74 A G					---		CCAGGAATAAAAGAAAAAGAGTCAGAGGAAACAGTCTTTGATGTTATAGGGCTGAGACACTACTC TTCCCTCA/JGAGCTATTTCTGACTATAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A					---		CCTGTCCATTTATTTGTGCATGTTCTTAAAGGCTGTGAAGATAACTTGAATGTGGGAAAC ACATAGATCCCAGA/JATATTAAAGGGCTGGAAGTAGCCTTAAGAC
WI-16644	42 G A			CAATAAGCAG CTCATTTTGAT TAC	CAATAAGCAG CTCATTTTGAT TAC	TATACC	CAATAAGCAG CTCATTTTGAT TATACC	AGAGCAATGGTGGATCTCAATAAGCAGCTCATTTTGATTAC/GJGGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCTCCACAGAACTTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGAT
EST12005 9	56 A G			TTGTATAATA ACACTCAGTA CAAAGTCTGT	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCTGGAT	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GCCTAGTAATCCAAAAGGAACATGTTTGTATAATAACACTCAGTACAAAAGTCTGT/JGJATCCAGG AAGTGACCAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTGAATC
EST12055 9	32 T C					---		GTGGAATAATTTTTATCTGTTACGCTCTTCCCTT/CJATTATATTATCTTGTCCCTGATTTCAGCACCC CACCCGATTTGCAGGCAGTCTTTCTAAACTGTGCCCTGTGAGCTGTAAAAAGTCTTCT
EST12492 1b	95 A G					---		CCCCTAGCAATGACTTGGAGTTGTGCCAATACCAAGTTACATACTGTGCCAAAAATTAAGCTCTC TTCCCCAGAGGCATTAACAGATTAT/JGJGGAAACGCACAGCAAAATTTGACGATGCGAGCTTTTA CCTTTTTA
EST12492 4	25 A G					---		ATCTTGAGGTTTCTGGGCTGTGAG/JAGJAGTGACATCTTTACTTACCACAGGTGAGAACCTAT AAAGAAACTGTGTAGAAAAGATATCAGGTGAGACTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAACCAAACTGGAGGCAAGTCCACAGGTACACTTGTCAC[C/G]CAGCAAGTAT AACAAAGTGGTTTCGATGAAGAGAAATGCTCAGGGGAAATGACCATTTTAAAGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTTATTATCCAAATGACAGTGTGGCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGC[A /G]TTGAGAATACAAATATTGAAGAAGAGTCACTGCCTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTGCATGAGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGGATGGGAATCCATGTTGCTTTGCGTACTCCATCAGGTCATTGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCAT[A/C]AACAGCCAGTTATTTCCACCAGAAATTTGTTGGGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACCTGTTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAATACCTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTCCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTTCTTAATGAAGCATAATAAACAGTTAAAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAGCAGCTTCCCACCCCAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTCTTTAAAAATTTAATCGCTTTATACAAATGACACCAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTTCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT[C/G]GACTAACCAAGTTCTACAAATTTACATATCCGTCAGTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTGCCTGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTGTGTACAGGAGCGGCTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT TCTCAGGCT	ACAAGAGGGTT TGACAAAAAGA G	AAAGATATAAAAAACAACCTCCCATCAGTAGCAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG CCTT[C]TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTGTATATAACCA

EST13278 2a	51 A G G	CATTACCGAA CAATATTTAG	CATATCTTGG GTGGTGAGAA	TTGCGAGAACGTTTTACAAGCTCCAAACCTTTTACCAGAACAAATATTTTAGG[A/G]ATTTGAAATAT TTCTGTAGTTCTCACCACCCCAAGATATGACAGCTTG
EST13282 0	99 A T AGTCCAAGA	CCACACATTTT CAATTTTGA	GATGGAAAAAT TGAGGAAGGT	GCTCACTAGATGAGCATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGCTGAATTAAGCC TGCCTGAGAATCCACACATTTTCACTCAAGAA[A/T]AACCTTCTCAAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39 A G CTT	AGTTGGGTTT G	TGGAATTTCA	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGGGCTTTTTG
EST13518 2	45 C G ---	---	---	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTGAGCATTTA[C/G]ACTTTAAAAATTAACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTCTGCACCTTCCCTTATAACCTTGATTG
EST13522 8a	66 A G ---	---	---	CAGGTTGGTGATTCTCAACTAGGAGCTATTTTGGCCCCCATCCCCCGGAGTGCTGGATCACTGGGTAGAGGCCA GIGTTTTGATTGTCACAACCTGCGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C ---	---	---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAAGGAATAAGGGAGAGGAGGTTCCGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G ---	---	---	AAGATTACGGACCATAAGAACTGCCCCCGGACCATACACACAAATTTATAGCAGGTAAACCAAA CTGAAAGGAACAAAGTAATGACTTTCTTGAACAA[A/C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G ---	---	---	CCTCAACCATCTGTAAACCGAGCCCC[A/G]CAGTGACCCGGGACTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G ---	---	---	CAATGGTGTCATGTGAACATAT[A/G]ACCTATTATCAAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAGTCATCTGCTAAAAATGACCGAACAGGAGGTAGGAGG
EST14221 5	42 T C CAGAGGCATT	GCAATGCTAGA GGAACAAGTC	AAAATATTTT AAAAGA	AAATCAATGCATTTCTTGGCATGCTAGACAGAGGCATT[A/T/C]TTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCTCCCTTCACACTCATTTTAAATTTG
EST14812 2	50 A G ATA	CAAGTCAGCTT CTACATTTCTGA	TAAAGATTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTTCAAGTCAGCTTCTACATTTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGAGTTTGCCCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T ATACITGGTT	CATCACCCACC GTACCCGAA	CGGGAAACA GTACCCGAA	TTTGCTTCGGCAATACATAGTGGCAATGACGCGTGAGTTCGCGCGCTCTCCCCACTGAACCAAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCAATCACCACCATACTGGTT[A/T]TTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---	---	---	TTTAAACCCCAAGACTTGTAGTGTGAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTGCATCATATAATAGCCAAAGGACTC/AJGGAAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GGTTTGCCAT GAAAAGACAA AGACAACAGA	GAATAGCTGA AACAGAGATA TTATTCTC	GTCACGACACTTTTATTAAAGACGTGAAAAGACAAAGACACAGAGGA[G/C]AGCAGAGAAATAA TCCTGTGTTTCAGCTATCCAGGATGTTATGCCAATTTATCCAGAGTCCTTGATCTGATAGTA
WI-16739	57 G A CACAAGC	GGTTTGCCAT GATA GTGATG	TTCAATTATCC CTATAA	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATGCTCCCAAGGT
WI-16782	96 C T CACTGTAAAGG TC	GGTGGGAGTCT GATAGTTGATG	CTTCTATCTTT CTGTTCCTCCA	CTTCTCCTTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATGTGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTACCTGA	CTGCTTGGTTC AATCCTTATTA	AAAAATGTAAACCTTAGAGGTTGCCTCTTTTGTGTCACTTTTCTCTGAGATGTCTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGATATTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---	---	---	CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTTAACTAAAGGTCAGGCAACATAGGAT[C/T]GTGA CAGCACCACTCGGACCAAGAGTGTGAAAATCGTCACACTAGCGTGCCAGCCCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---	---	---	GGTTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATTCATTTTGAGAGCTGTTTTGICAGCC TTTTCCAGAAAAGGCCGCTC[G/C]GGGTTTTCTGAACCTCTATGGGCAATTTTAGAAT
EST16089 9	96 C T ---	---	---	CGTCTGAAGTTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAAGAGCCATCCCTGCCCCCTTTCTTTGCT
EST16100 1	24 C G ---	---	---	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACACAGTCCATTTATAAGGGGTGTCACATTCOCA GGGGCTCCAAATAATGCAACATGTTTCACTCGTCCATGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTGGCTC
EST16104 9a	83 A G ---	---	---	TTCTTTTAAATAACCCACAGACCCCATGACACTTCCAAATTTACAGAGCAAAAAGTATTGCGAG CTGGTTCTCCAGGGA[A/G]TTGGCCCCGAAGCTGGCTCAGTTCACTCCAGGACCTCAGTC
EST16118 0b	119 T C ---	---	---	ATGGTATAACAAAATCAGTCCAGGTTTTTTTCTGAACAATGATCCTTTTCCCGTGGCATG CTCCTAAAACAACATAAAACAACCCCTCTACGCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---	---	---	ATGGTATAACAAAATCAGTCCAGGTTTTTTTCTGAACAATGATCCTTTTGGTCTTTCCCGTGGC ATGCTCCTAAAACAACATAAAACAACCCCTCTACGCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---		AGCCAAATTCAAACGAACCTCTATCAAAACACACAAAGGCCTAGAGGAGAGATTAC/TAATGAACGTA AAATAATTCAGGGCAATTTTGATCTAAAGCAATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTTGATAGGA
EST16182 6	54 G A ---		CATTGGTTGGTAGGGAAGATAGTAGTGCAAAATAAAATGGTAAACACAGCAG[G/A]AAATGGAA TTATAGCTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGCGAGAAGTAGTA
EST16183 2b	59 A G ---		GCAGGTAACACTGTGGTTCCAAACGATTGTTCTTTTCATAAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTCTTCCTGGCCCTTCCTCGTTTCATATTTTATGTCACTGTCTCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---		AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTTCGCATTTT CCCCAGAGGAAAAGTCAGCATATAAACACACATGGGTACATGCTCAGCACATGGTGTC
EST16229 2c	52 T C ---		TGTGAACCTCGAATTCGCTTGCCAAGTCTGAGTCACAGTTTCATTTGGGAGT/C/CCCTGTGCAGCC CTTGCCAGTTTTCCAGGAGGAGGATACTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---		TGTGAACCTCGAATTCGCTTGCCAAGTCTGAGTCACAGTTTCATTTJGGGAGTCCCTGTGCAGCC CTTGCCAGTTTTCCAGGAGGAGGATACTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT	CAGACTTTTCTCACACCTCATTGGCTGGAACCTGGTCACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGGTGCATCAAAATTCCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA[A/G]ACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49 G A ---		GCCACTCTCTGTGGCTTGCTCTGTCCAGCTGCTGCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAGCAATTTAGCCAACTCTGGTCTGCCACTCTCTCTCTCCGCCGCTGGGGCTCACCCACC TCTCTCTCTCAATC
WI-16824b	83 G A ---		GTACCCCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTCTG	GTACCCCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT/CJGTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGCTTACACCTTTAGCACGGATAGTTTCCTGGTCCCAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---		TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTTCATTACAAA AATGGCTTCCAAACCATTAAAAATGAAC-TT/CJGGAAATAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TATAATCCATCCTCCAACACACACACAAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTACAAAGACCTGTGCTTCAAAATGTTTTCTCGATAATGTGGAGAAATCTGCTCTTTATGTA

-201-

WI-16879	79	C T	GATACAGGC ATAATTTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAAACAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCAIC/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCACCCAG
WI-16882	99	A G	GAATGCGCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAATTTCCCCCTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTCTGACIA/GGCGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70	G A	GCTAACTTTGG GCAGGTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGAGAGAGAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C T	ACTGGCCTGT GTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTGTTGTTGTTATTTGCCTCCCAACATCAGAACATAAGTTCCATGAAAAACAGGAACCTTTGGCCTGTG TTGTTCA[C/T]CCCACTGCCTAGAAAGATATAGACA
WI-16910	74	G A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGTTATATTCGCTATGACTTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA[G/A]GTATCTGTATAGAAACGATACCTTCATTTGGCCTGAACCAAGTGAAGGT
WI-16918	93	C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATCTCTCTGCTACACAGAGCACTAAAACTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC[C/T]GATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGTCTCTGAAAG
WI-16947b	127	A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG[C/G]ACAGG TGCGTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG[C/C]CCA CGGGCAATCAGATGAGATG
WI-16947a	58	C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43	T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAAACACCCTAATA[T/C]CTTAACTTGGTCCAACCTATTT AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAAA
WI-16995	55	T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATTT[C]ACGGCTGG AAATCAACATGCCTCTCTTCTGTGAAGTTGTCAGCATGGAGCTGAGAAAGGCTGAGTCAATCT
WI-16992b	60	T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGT[C/G]A]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTGGGGTTTAGGAA
WI-16992a	46	G A	AAGCACCAG AAGTACACTG TC	CACATTCCTT ACAGTCCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGT[C/G]A]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTGGGGTTTAGGAA

WI-17010	23 T C	TTCACAGGA AAAGCCATG	AATAATACGGT GTTTTGAATGT CA	ATGTTTCAACAGGAAAGCCATGT[C]ATGACATTCAAAACACCCGTATTATTAGAAGCTCATTTAAT TGTTTTAATGCAGACAAAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTCCACG
EST17127 9b	74 C T	CACTGGCAC AGACAGAGT	GGGAGGGCAGG GGTG	ATTCGGTCTCCAAACAGCATCCAGGCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA CAGAGT[C]TJGGGAGCCATGGGCACCCCTGCCCTCCCAAGGCTTCCTAAGTAACAACCT
WI-17040	94 T C A	AATTCTTTAT CATCTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGGCTTCATTAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAAATCTCTTATCATCTCAAGCCAGT[C]CATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTCC AAATCTTTCATATGT
WI-17044	47 G T G	GCCAAGGGAT TAACGTATAG	GGGATCCCT TGTTAAGA	TTGTTTGTGTTTTCTCTCTCTGCCAAGGATTAACGTATAGG[C]TCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCTGCAGAAATGGCAGGAATCGAAT CAAAAAGAAAAGCAAGTG
WI-17021	62 T A ACTC	TGGACTTGCA GCCTATACT	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCCTATAACTACTC[T]A/G CAGCTGCCACTAACTCTACAGGCACAGTAACACTACACTTTATACAGGAGCACATGCCAAAGTGCCTGG GAGGTGCCAATAAATCAA
WI-17065	90 T C CT	CCAGAAAGGA AAAGCATAAA	CCCAAGAGAC AATGAAATCCT	TGTAAAAATGTAGACATGGGGGAAAAACATTGTAATCAACATGTGCTGTTTTCTACTCCGGTA CCAGAAAGGAAAGCATAAACTTT[C]AGGATTCATTGCTCTTGGGT
WI-17066	32 A C T	TGTACAGCCA ACATCACTGTT	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCAAACATCACTGTTT[C]ATTCAGAAACATTTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCATCCCTGTAGCTTCCTCATAGGCAATGGCAATGGCAACTGCTGATC
WI-17074	86 T G ---		---	TGCTGACTGTCATGACTTAGTAAGGGCATCACAGGTGGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCTCCTACACAGGCCTT[G]CTACATAGGAGTATATTTGGCCAAAGACTCACCCTAGAGTGATT
WI-17104b	108 T C ---		---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTCTGATGCTTTCCGAGCTTTCCCATTCATCCA AATCAGAAAGCAGTCAGTGGCCCCGTGTTTCCAGACGGCTT[C]TCTCTTTGTTAAGAAATTA
WI-17114a	37 T C GACTTTGTTT	TTCCATCAAG GACTTTGTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGATGTTTCCATCAAGGACTTTGTTTTT[C]GTCTCTCACTCTGCTATTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAAAGAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76 T G CTCT	GATGAAATTC AGATAGTCTTC CTCT	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC TTCCCTT[C]TJG/CATATCTTCCAGGATCTGAGAGGGCCCTCTTTGTCTGCTCTAATTT
WI-17163	43 A G TAACGTT	CATTCTTTGT AAAAATAACAA	CAGAATCTTGC TTTTGCCTT	GAAATCGAATACGTCCATTTCTTTGTAAAAATAACATAACGTT[C]GIAAGGCAAAAGCAAGATTCG TAAACCAACATTGGAAAAGGGACACAGGGGAGGGGAGGAAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA

WI-17178	127 T C	GGACTCCCTCA	CCCTCAATTTT CAACTGCTTC	AGCAATGTCCTCCCAATTTTCATTAGCTATGATGGAGTTATCAGTTTCATTTTCAGAGCGAAATTACTGG GGCGAGGGGGTTTAAATATCTGATGGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA GCAGTTGAAATTTAGGGG
WI-17180b	81 C G	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCCTGCACITTCCTCCCAAGTCTCGTCGCACAG GCTTCAACAAATTAAC/JG/AACATCTTGCCCAATTTGTTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17180a	47 T C	CACAAAAATA TAGAGAATCC TGCA	TGCGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCCTGCACITTCCTCCCAAGTCTCGTCGCAC CAGGCTTCAACAATTAACCAACATCTTGCCCAATTTGTTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17156	54 G C	TGTTCTCTAAA CTTTAGATATC TCCCA	CAAGAAATAT ATATTTGATTC TGTGGAA	TGAGGTAGCAGGGCAATCTTAAGAAATGTTCTCTAACTTTAGATATCTCCCATG/JTTCCACAGA ATCAAAATATATTTCTTGTTGGAAATTTTAAATGTTCTTAACATCTGCCTACCATCCACCTCAAT TAATATCTTG
WI-17149b	79 T C	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCA/T/CJGTGTATGAACATAAAAGGATGGGAAAGAACACATTTCTCACA
WI-17149a	48 C G	CAAGGTTTGA AGGAGGAACA	CCACGCACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTGAAGGAGGAACATG/JTCATGCACGTGCGTG GAAACCCAAATTTGTCATGTGTATGAACATAACAAAGGATGGGAAAGAACACATTTCTCACA
WI-17197	67 G A	GCAGAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCTCCTGCCTCAGCAGAAGTAGTGGGGCTAC/JG /AJGGTATGCACCACTCACCTGCTTATCAGTTTCGTTTAAATAGAATATTTGACTTTTAGATGCGCA TGATTTTCAGTACTTTTCTCCCTTGTCCCTAGTTT/JC/JAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGACACATCC TTC
WI-17198	38 A C	CCTAGTTT	ACTGAGAAATT	TCGCTATGCTACCCAGGCTGGTCTCATC/JTTCAGGCTCATGGATCCTCCTGCCTCTGCAGTGGCTGG GATAAGACACAACCTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
EST18753 8	27 C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCCTGA	TTATTTTAAACATAACCAAGATGCACCTTGGTTTTTACATTCTCTGGTTGCCATTTCAGTCTCAAAGT AAACAC/C/JTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACTTACAGAGT
WI-17108b	74 C T	GCCATTTCAGTC TCAAAGTAAA CA	AACACGATTT ATCATATGCTC CC	ACACAAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JG/JTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCATCACCATTTCATCATCTCCGTT
EST19067 2b	41 A G	ACACAAAAATTTACCATCGTGACCATTAAAGGGTATAGTTCA/JC/JAGTGGCATTAAAGTACATTCAACT TTTTGAGCAACCCGCCATCACCATTTCATCATCTCCGTT
EST19067 2a	40 A C	CGTGACCATT AAGGGTATAG TTC	AAAAGTTGAA TGACTTTAATG CCA	CTGTTTCTCAGAGATGACACTGCCAACAJA/JTTCACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAAATTTACAGTAGTGTGTTTTTCTCTCTGAAAAA
EST19125 8	28 A G	

EST20824 8	115 T	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGAAGCCGGAGTTTATTATTATTCAATCAGTCTCTCTGAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGAGTGCTGATTGTTGTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCTT[AG]GTAGCACAAGTGG ATGCTTGAAGAAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTAGTGGGACCA
EST21904 b	128 G	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGCAGTTCAGTGGAGGACAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAGAAATGTACTAGGCTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T	GAAGATCTGT CTGGCATTCTT	TGGAATAACA GCCCCAC	CAACAAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGCTGGCATTCTTTTCTGTTGGGGCTGTTTTTCCAAGGCACA
EST22197 2	78 T	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCCTCACCATAATCCACAGGAGAACTCTTAATGTTTACAAGCACCAATTTATTCTGCT ATTCTGCCCATT/CJACCCGCATCCTTCATGGTAGAGTATCACAAGTAAAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTTACTCTA[T/C]JGTCAAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCJAGJCCACTGTAAA CAGTAGCATTCATGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATAT/CJACATAAAAAATCCACCACCTGTAAA CAGTAGCATTCATGTTTTTACTCTATTGTCAAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A	---	---	TCGAGGAGCTCTGAGGAGC[C/C]CACCAGGGACGTGTGTCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTTCTCCTCCTTTACAAAACCTCAGCCTCACCCACACAAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTAACTGT
EST22433 c	103 A	AAGACATGTT CACCAAGTGA GAA	CAGCTTCAGCT TAACGTGACAGA T	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCAGAAAGCTTTACC[C/A]GTCTGTCAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A	AAATGGATCC TTATCTGCACA	AGTTTCAGTTT GCATGAATTTT T	TATCCATTTCAAGAAAAAAAATGACTTAAAAAATACAAATTCATCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTGTT TCTACCCC	TTGCTGTAA TTTGAAGTAA TG	GCCTTTTATGTCCTTTTAAACATCAAAATGTTTTATAACACACTTGATCCTTTTGTCTACCCCA ATT/C/CATTACAGTCAAAATTAACAGGCAATATAATAGGTCTAACAGAAATGCTTGCAATT TTATTTCTCAGCTTACCAATTTGTGACTTATATCTCTGTACAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAACTCTTGCCCTT/JATGGTTTTGACAGTTTGTGTCTTTCT T
EST23021 0	108 T A	---	---	ACAGAAATTTAAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATAATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGCACTAGGCAATGTAAGCTCCAGAGGCAG[C/G]CTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTTCTTTTCTT/GJTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATGAGGCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAA CTGACAGTCCCTGTGTGCGGGGTGCTCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTCC
WI-17387	55 C G	CCTTTGCAGAT TGAAGAAAA	AGATTAATAGT AACTACT	ACAGAAATTTAAACATGCAAGTTTCATTTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATAATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTTG TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGCACTAGGCAATGTAAGCTCCAGAGGCAG[C/G]CTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTTCTTTTCTT/GJTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATGAGGCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAA CTGACAGTCCCTGTGTGCGGGGTGCTCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTCC
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGCACTAGGCAATGTAAGCTCCAGAGGCAG[C/G]CTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTTCTTTTCTT/GJTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATGAGGCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAA CTGACAGTCCCTGTGTGCGGGGTGCTCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTCC
EST23733 9	31 T G TT	GGCTGTAGTT TTGTTTTGTTT	TGCACTTTAA TCCCATCAAT	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGCACTAGGCAATGTAAGCTCCAGAGGCAG[C/G]CTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTTCTTTTCTT/GJTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATGAGGCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAA CTGACAGTCCCTGTGTGCGGGGTGCTCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTCC
WI-17470	83 A G	GTCCGTCCCG CCAG	CCAGTGAAGG GCGA	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGCACTAGGCAATGTAAGCTCCAGAGGCAG[C/G]CTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG AAAGGCTGTAGTTTGTGTTTTTCTTTTCTT/GJTATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATGAGGCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAA CTGACAGTCCCTGTGTGCGGGGTGCTCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTA/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTCC
WI-17519	55 T C A	GTGTCCTAGC TAATGAATGC	AATTATTATTT TGCAGGCAATA CTC	TTTTTAAACGAAATCTCACTACTGCAAATGCATTTGTTGTCTTAGCTAATGAATGCAT/CJAGAGATTG CCTGCAAAATAATAATTGAGATTCTATTTTTAAGAAGCTTAGAACAGTACATGGTGCATAG TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTG TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACACATT ACTACCAAGTTATTGATAATGATAGAACCCAA[C/J]TAGGGCAAATTTACATTGACGCGTCATGC
EST25356 3b	95 C G	---	---	TTTTTAAACGAAATCTCACTACTGCAAATGCATTTGTTGTCTTAGCTAATGAATGCAT/CJAGAGATTG CCTGCAAAATAATAATTGAGATTCTATTTTTAAGAAGCTTAGAACAGTACATGGTGCATAG TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTG TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACACATT ACTACCAAGTTATTGATAATGATAGAACCCAA[C/J]TAGGGCAAATTTACATTGACGCGTCATGC
EST25356 3a	26 A C	---	---	TTTTTAAACGAAATCTCACTACTGCAAATGCATTTGTTGTCTTAGCTAATGAATGCAT/CJAGAGATTG CCTGCAAAATAATAATTGAGATTCTATTTTTAAGAAGCTTAGAACAGTACATGGTGCATAG TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTG TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACACATT ACTACCAAGTTATTGATAATGATAGAACCCAA[C/J]TAGGGCAAATTTACATTGACGCGTCATGC
WI-17581c	99 C T	---	---	TTTTTAAACGAAATCTCACTACTGCAAATGCATTTGTTGTCTTAGCTAATGAATGCAT/CJAGAGATTG CCTGCAAAATAATAATTGAGATTCTATTTTTAAGAAGCTTAGAACAGTACATGGTGCATAG TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTG TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACACATT ACTACCAAGTTATTGATAATGATAGAACCCAA[C/J]TAGGGCAAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGATAA	CGTCAATGTAA ATTGCGCT	TTTTTAAACGAAATCTCACTACTGCAAATGCATTTGTTGTCTTAGCTAATGAATGCAT/CJAGAGATTG CCTGCAAAATAATAATTGAGATTCTATTTTTAAGAAGCTTAGAACAGTACATGGTGCATAG TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTG TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACACATT ACTACCAAGTTATTGATAATGATAGAACCCAA[C/J]TAGGGCAAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CATCTTATAG CTAGAAATCGA CAATAT	TTTTTAAACGAAATCTCACTACTGCAAATGCATTTGTTGTCTTAGCTAATGAATGCAT/CJAGAGATTG CCTGCAAAATAATAATTGAGATTCTATTTTTAAGAAGCTTAGAACAGTACATGGTGCATAG TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT TCTTTGATACAGGTAACCAAGTTTGTGTAACATTTATCAGAACTTCACTGTATCTTCAAGTTTCTTTG TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCAACACATT ACTACCAAGTTATTGATAATGATAGAACCCAA[C/J]TAGGGCAAATTTACATTGACGCGTCATGC

WI-17623	46 T C ---		---	TGTGGTTTTAAATTTCCATATAATTAATGGTGGGCACATTTC/GCATGTGCTTACTGGGTC ATT CATATATCTTTGTGAAGCATCTGCTCCAATCTTTTGCTGACTTTGGAGTTTTTTGGT
EST26419 1b	46 T C ---		---	ATTT CATACAGAGATACAAAAGGCAACTATGTGCAGCAACAATCTGA[T/C]GGGCAGTCCAAAATTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC	CAAGAAGTTTG GACTGCCC	ATTT CATACAGAGATACAAAGGCAACTATGTGCAG[C/A]AACAACTCTGATGGGCAGTCCAAACTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAAATG
EST26780 5	69 G C ---		---	TCAGCTTTAAATTAAGGGACATGTAAATAAAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAGAGC AG[C]AGGTAGACCAGTAACAACAACCAAGAAAGCAAAAGTGCCTCGTTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---		---	TACTCAGTTTAAGGCAAAATCCACACAGAGACTGTCTC[A/G]GAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---		---	CAAAGGATTTTATTTGTTCCCTAAAAAGTAAATCTAGAAAAATAGCAACCCTGCAAGAAGAGATT CTATAC TAAAAACATTTCAATCATCTCTCTCTC[T/C]TTTACACATGGTGACTCTTTTCATGTACACAT CATCGGAAAAACAGACTGA
EST27504 0a	33 G A ATTT	GCACTTTGCA CAATTTAATA	GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACTTTGCAACAATTTAATAATTTATC[G/A]CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTACACATCTGTTAACAAGAACCCCATACATT GGTAAAAATTCATCT
EST27662 4	51 C T CTCCAGTCTTG	CACATTCTGTT CTCCAGTCTTG	TTATGAAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTCTGTCTCCAGTCTTG[C/T]AGGTTACATAAG CCATTTCCATAAAATCTATAGCCTCTCTCTTAGAGTAACACACACTCTTGTTTAGGAATGTC
EST27788 3	100 A G ---		---	ATTTTATTAGCGGTACAAATCCAAAGGTGGTAAGGGTGAAGGAAAGGAAAGCGAGGCAAGCAATACAT TATTGAGCTGA AAAACAAC TTTACATTCAAGGAC[A/G]GCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC	GTGAGAGAGG TACTCCAAGTA C	TCCTCTAAACCTTCTCTCTGTGGATCCCAGTGACGTGGGAAGTCATCAGAACCCCACTG[A]GTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAAATTC AATCTGTAC	TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTCCCCAATGTAACAATAAAATTTCAATCTGTACACAATC[G/A]AAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---		---	TCCCGCTTCCAAAAGCTTTATTGGCAAATATGCTCTA[T/C]AAAAAGAAATGATCAATCCTGTTCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACACCACCGCGTGTGAAGGAGAGACTGCTGTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTGCGATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTTCTTTAAAT/AJATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGATGTACAGACAACAGACGAAGACATGAGTTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGCGCTGCC TGTC	TGGGTTGGCAG TGTC	AGAAITGGTCTAGTAATCGTTCAGGATTCGGTGATGGGCCCTCCCTGTCT/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGGAGAAAGACCACAGAAGTGAAGTGTCTATTAGTTACATCATACCAAGTGTACATACTG TT/CJACATGATTTATGGCTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGTCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACCACAGAAGTGAAGTGTCTATT/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTGTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAACACATTAAGCATCATTTGTCACCT[G/A]GCTAACTCCT CAAAATCAACAATACCCCTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTAGAGGACACACCAGTCTTGTGGACTTAGGGCTACCCTATCCAGCAGGTGCCJAGJTATTT TCACCTGGTTACGTCTGTAAAGGACCGTTTCCAAATGAGGTTACAGTCAACAGGTTCTGAGCAGACATGA GTTTGTCTGGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTG TCATTCTCTG T	ATTTATTAGTATCTGCTGTTGGGGTGGGTGGGAGATTGTTTGAGATACTGCAACAGACACAAA AGCAAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAGAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATAATTAAATCTTAAAAGTTAACTCACCATGA TTTAAOCTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTTAAATTC[C/A]G/GGATTTAATTTCTTCTAGTTCAATCTTGGA GG
WI-16260b	86 G A	---	---	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCACAATATAGGTAGC[G/A]ATAACCAGGTCTCACTTTCCCTTCCTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAA[G/T]ACCC AGAGTTTCACAATATAGGTAGCGATAACCAGGCTCACTTTCCCTTCCTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTCCTTTCTTG[G/A]GCCTGTTTCCTATACCCCAATATCATAGAATT GTTGTTGCTTCTATAATGTTGAGCTTCAAAATCTTTTGTCTAATCAATCCAAATGAATTACCTGAATT TTCTCCTCTGTTCAAAA

EST31951 4	87	C T	GGGTTGTCAG CCAACA	CCACCAAAAT CACCTOC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAACATTTTCACTCTTTAGCAATGACA TCGGGTGTCAGCCAAACA[C/T]GGAGGTGATTTGGTGGGAATCTTATCACAATATTCT
EST31968 8b	95	T G	---	---	CGAATTTGTCCTCTTATTTTGATCTAGTAATCCTAAAAGATTTGGGGGCGGGTTACTATAAGT GCAATTTTATAATGGGGATTTTCTGCTT[G/A]ACTGCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCCTCTTATTTTGATCTAGTAATCCTAAAAGATTTGGGGGCGGGTTACTATAAGT GCAATTTT[C/J]ATAATGGGATTTTCTGCTTAAGTCCCCTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACCTCCCTCCGACCAGATGCTGTGGCCAGAGC TGGCTTCCCCTTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTTCAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---	---	AAGGCTTTCCAAAGCATCAAAGGCACCTGGGTGTTGCTCTAAGTTTCTGGTCACTGCAGCCCC[AG JTCTGATTTAGGGAGCACCCCAAGCCCAAGTAAACATAATGGTTCTTGCAG
WI-17800	29	C G	GGGAGCACAA GAGAACTCA	TTTCTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAAACTCAGT[C/G]AAGACTGGGATTAATTGTAGGAAATATTTTCACAG TTTCCAAAGTCAGAGAGCTAATCCCAACCCTCTGTATCTGGAACATACACTGCTGGCATTTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCAATCCTAAAGTCTGGGATGACTTTCCT[G/A]TCTACATCAAGTAGAACCTAAGCCAAAT TCAGAAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACTCCAAGCTGAATTAATGTTTCAATCT
WI-17860	121	T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAAACAAATCTTTA TAGTGCCAAAGATAAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAAATAT[A/J]CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	CAGCAACCTTTTTTTTGTATAGCCTACTTCTCAAAATTTGTI[A/T]TTTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAAACTACCA
EST33301 4c	80	G A	ATTGTT	---	GAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCCTGATTCCTCACACAAGCATGATC AATGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAAGTCAAAATGTTTCCCTTTATGGGTGATGCCACCCTGATTCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A CA	AGCGTGGTTTT CAACTACTAA	CTGTATTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCGCGGTGTTTCAATACTAAACA[G/A]GTAAACAATGCAAAATATT TAACAATAATACAGTGATTAAATAAGCCATGGCATAICCCAGTTGATGTAATACTTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC GG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACAC[A/G]TACGGGAATTAC TATTAAACATAAGCGATAACATCAAAACATCTGTAATATGCAGTTAAACAAACACAAATGA
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAACTA ATAAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAAATGTGTGCCAAATACTCAAGTGTGAA TJAGJGATTTTATTAGTTGTTCTCGCTAGTAGTTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAAACATAAGTTAACTCAAGAAATATATTCCAGTCTTTATGTTACTAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAACTTACCATCAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATAAAT CCTAAAGC	CAGAAATTATG TGATAATACT CCTTCC	GGTACACAATTTTAAATGGAAGGAACACACAGGTATGTTGAAAGAACAATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCCTAAAGC[C/T]GGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACTCCGGTGATAATCTGCCATTATTGATTATTATGATAAAACACCTCTCATTGTGA AAACACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATGT[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84 A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAAACAACATCTCCCAGGCCCTCGCAGT AGAGGCGAAGGGAACAG[A/G]GCTGCCCATGTGCTCTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G	---	---	ATTCTTTATAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAAGGTGCTCTTCC[A/C]GTTTCTAACTCCCTGGACTCCCTCATTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G	CACAGCCTGC CCCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCC[C/A/G]TCTTGA GATTCAGAAATCCAGAGGGTGCTCAGTCCCTGGTTTAGGTGCTTCTGTGACATTTCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATC[T/C]TGGTTACACATCTT A/GJACAGCAGAGCTGCCTGAGGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	CCTGAGTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATC[T/C]TGGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGGG GAGTAAAA	CGTCACCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA[A/G]ATGGAAAGCAGGGTGACG CATGCGAGGAGTCCAGACAAAAGACGGGTGATTTTGTCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54 G A	GTAGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGTGGCAATCATCTCTCAAAACCTGTGGGTAGCTGCTAAGCTGTATTTTCAGAG/GA/AAATGTCAC AATCATACCACCTGGGAGAGAAAGAGTAGACAGCTGCTTATTAGGTGCCAACTGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCACC TGCT	TTTAGCACCATTCTTAGTGAGCAGGATTCTTGATCATGGGTGGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAGT/CJAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C	AACCCACTAC TTACTCAGAGT GTGTAT	AAAACTAATA AGAAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTGTAT/CJATATTACACATGAAAGATATAATCTTAGAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAGCATTTTAGGTGCAAAAGGATATAA
WI-18080c	80 C T	---	---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCGGTG TTTGACTTTTAT/CJTTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65 G A	---	---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCGG/G AJGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41 T C	GCAAAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCT/CJTTGTAAATTAATCTACTATGCG CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18086	63 G A	---	---	GTGGGCATCCTATAAAGCAGCCCATGTGTTGAAACAAATGATATGCACAGAAAGCATACTTCT/GA/] TGGCTTTGTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCGAGTCTAGC TTAGGAGAGGTGTTTGAA
WI-18115b	71 C T	---	---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTAACCTTTGGTATCCC TT/CJ/TJTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T T	TTAGTGACCT TTGGTATCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTAACCTTTGGTATCCC TT/CJ/TJTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAGAAAGGGGTGAG TCAGT
WI-18136	78 A G	---	---	TTTTGAGAAGCACTCTGTAGGCAAGGATGCATTCAAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTGC/GJTAAGAACAAATAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115 A G	CCATCTTTCCG	GAGTTCTGCTT	GGCAAAATATTTTACATCACACCTGGAAATCTGCCCAAGTCTTTCCACTATGAAGGCAATCGTAGAG TGTGCGAGGAGGAAAGGTGTTATCCAAAGCAGCCATCTTCCGGAAGCTC/GJ/JGGAGCACAAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26 G A	GAAGCTC	GTGCTCCA	TGAAAGAGTCGACACAGCGGACACT/GJ/ATCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAACTCTGGCGA

-211-

WI-18190	62	G A	---	---	...	TGAAAGAAGTCGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAAATCCTGGCGA
WI-18181	100	A C	CAGATC	AAATATATAC AACACTCCCTT	CGTTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACACATTGAAACACAAATACAACAAAAACATTAGGAACAAAGAAATGTGTAATCCAA TGTTGAAAAATATATACAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTTCTTGAAC
WI-18215	78	G A	CTGCCCTC	AGCAGAGTTC	CCTCCCTCTCT CCCC	ATTACATACAGCATTTCTGAGTACAAACTAGGGACAGGTATTTACAAAAACAAATAGAGCAGA GTTCTCGCCCTC[G/A]GTGCGGGGGGAGAGAGGGGATTACGCAATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCTCTTC
WI-18232	60	T A	AA	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT C	CATTTCCGAAAATCTGATAGTTAAATAATCCCGTCTGGTGTGATTGTGATACACTTAAG[T/A]GAA CCCTGAAAACCTTTATTTGAAATTGAAGTTTTGCTCAGAAAACCTGGCAGAACCTTTTCACATTCTG AC
WI-17892	76	T C	ACA	GGAAAACCTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACCTCTGTGGCATTTCGGCAGAAGTGGC
WI-18242	30	G A	AATCGTAACA	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAAACAG CTTTC	AAATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTGACAAAAAT TGGATGCCACAACCTTATCTCAACCTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCTATATC TGAAAAGATCGAACAAAG
WI-18266c	119	C T	---	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T C	---	AAATAGGAAA TATGGACTATC	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C T	TTCAAA	GCTGTCAGCTA TTGTTATTTCA	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A G	AA	GGAGAAAAGG GAGCAGAAGA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTGGATATGTGGTTAGTGTCTATCATTAATTTGGAAAGCTGTCAGCTATTGTTATTTTC AAAT[G/T]ATCTCTGCTCCCTTTCTCCTTTTCTGGGATTCTCATTTCTGATGTGTTATA
WI-18330b	66	A/G	---	---	---	AAACATCTACAGCTGCTTAGGCCATCCTGTGAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGGI A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATATAAATAAGAACATAATTTTTTGTGAT TCACA

-212-

WI-18330a	49 G A	TCCTGTAAGA AATCAGGGAT AGA	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAAGAACATAATTTTTTTTGTGGAT TCACA
EST37564 5	85 T C A G A	AAATTCAAGC CATCTACAAA C A G A	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGAT[C]TCTCATTAGGCTCCATAGGCTGCAACACATCAAAAGGCATTAC TGTA CTGGAGAGGACTGAG
WI-18327	104 G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGCGAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTTCGTTAGGCTAGT[G/A]GCTGAGCCATTGATGCGGAGGCAGA GT
EST37624 6b	102 G A ---		---	GTGGCAAGAGCAGCTAAACACACTCAITTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTGGCTCTCTGGACG[G/A]TTCACTTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58 C T ---		---	GTGGCAAGAGCAGCTAAACACACTCAITTTGCATGAACCTCCAAATACGAACAGTGCAC[G/T]GCTGA TGGCTGCAGTCTCTGCCGTGCTGGCTCTCTGGACGTTTACCTACATGGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89 C G G C A T C A A	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTAAAGTCTACCGTGTGAGTGCCCATGAAGCCAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCAA[C/G]TCATCTTCACTTTGAGTCTTCCAGCCAGGTCCTCAAGCTT GTGGACACAGACAAAGCC
WI-18012g	117 A G ---		---	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTGCATCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113 G A ---		---	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTGCATCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112 C T C C C T T	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTGCATCTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46 T C ---		---	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTGCATCTCCTTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75 A G C T C T G C A T T G	GCAAAAAGGA CTGATTATAA	GCTAAAGTCAG CTGATTATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTG[G/A]TTAAGTTTATTAAATCAGCTGACTTAGCATTTGGAGATTATCTGGAT

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAAACTGACCCAAATTTGGTAAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCGTTGCTTCCAGAGTGCAGTGATACTGTTATAGCC
EST38519 0	24 C T T	OCTGCAOCTCC TAAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGCACCTCCTAAAAGATCTTTTCCTCCCCCAAGTCTTAACAGAATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGATTGTGCTCTCTGTTTCAAGCTTTGATTTTTTGTCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1	66 T C A A	GAACATCCCA TGTTCTGTTT	AGGGAAGGTA GTATAACACAT AAGAGA	AGTGGTCAAAATGTAAAACATAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA TCTCTCTTATGTGTATACACTACCTTCCCTTCTCTTCTTCTTATACACATAGATTTTCTTAATTGCAGC CCA
EST38616 9	101 C G C T T C	OCTGCTCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGCAAGGTAACCTGAGCTCTGTGTCTCCAGAGTGGTGCCTCACGCCGGGGCCCGCTGG AGTCTCCGGGGCCCGCCCTGCTCGGCCCTTCCTG G GCCACCATCCATTCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAACCTGGG CATTTCAA	TTGCAAAAAATG AAGGAAAAA	TATAGTAGGTACTTTCTTGTCTGCAGCAGGAATTTATCAGTCTGAACCTGGGCATTTCAA T C GCGTG GTATTTTTTCTTTCATTTTGCAGAGTAAAAAATCAT
EST38654 5	42 T C G T T T T A C A	AATGGTCATTT TAATATATCA	CAGTGAATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTACATA T C JAGATAGAAGATTAAGGACCAT CACTGAGGTCACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGAGTTGGTTCCAGCATATA
EST38707 9	75 A G	GGATCCTCACTCACTCCCTGGGACAGCCTGAGAAGGGACATCCACCAGACCTACTGATCTGGAGTCCCA CGTCCCC A G AGGCCAGCGGATGTGTGCCCTCTCTCCCAACTCATCTTTCAGGAACACGAGG ATTCTGCTTTCTGGAAA
EST38759 2	86 A G G G T A T A T G G	TGCTCCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTTCTACCTAGAGGGAGAAGAAATCACCTACCTTTTGGATGCCCTCCACTCTACTTGT CTCCCTGAGGTGATATGG A G JCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATCAAA	GACTCTCAACCAAGAGAAAATCAATAGGAGAGGATTGGCT A JTTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACCTTATGTGTTCATTCAACAAG TGTTTATGAGAACCATTACACA C A AAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T T G A C	CACGAGTAA AAGAACTCA	GGAGCGAGTCC AAGAGAA	TCCTTACTGTGCTTACAACTTTCTCCCAAGTTTGGGGTGGTTTCCATATGTTTATGTTATGTTATTA TTCAACACGAGTAAAAGAAACTCATGAC C T TCTCCTTGACTCGCTCCTCCCAATCTCGAT ACCGACTGCACTGTTG
EST38865 2	72 T C T G T G C G A T G C A G G A C A C A G	GCTGTAGAATT TGTCCTAGTTGTTAA	GGAAGGACGG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGCT C G CTGTGTCCTCCGTCCTTCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAACCAAGTAATTAAACATCACTACTAGCCTAGATCCCTAAATC/TGAGGACATGAGATTT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAAAACATTCCC TTATTCATGTGTCATCTCACACATCTTTATTTATTTGTTTCACTTTCTCAATATCGGATTGTTGC TCATGAGAAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCA/G/C/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TTATTCATGTGTCATCTCACACATCTTTATTTATTTATTTGTTTCACTTTCTCAATATCGGATTGTT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCCTTAT TTTT	CGATATTGAG AAAGTGAAAA CAA	
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTGTTG ATTCCCATCTT T	GCACTAACTAACTTTTCATTTGTGGATTGACAGCATGGCTAAAACG/G/JTAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	AACTGAATGGCAGTGAACACACTACACATCAAAACTTAGGGAAATGTGGTTAGTGTGACGTTGAG GGAAACTTATAACCTCAC/G/JGCTTTGTTTCACAAAACACAGCAGACACAGAGATTTTCCAACTC CAGCAATGACAGGCTAGG
EST38955 5	30 G C	TGAATCCCTT GGTGG	CACTGCAATCT CAOCCCC	TAAACATCCCATTTGAATCCCTTGGTGGG/G/CJGGGGGGGGTGGATTGCAGTGTCAAGATAAA TATCACAATAATATCAAAAACCTTCAAAATGTCTATGCATTCACACACTGACATGAGCCACAAAACAT CCTTTCACAGGACTGTAC
EST39002 0	42 G A	GGACCCCTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCGGACCCCTCGGTGAC/G/JCAGGCTCCCTGCCAGGGCTGG CCCCTGACCGGGCTCCCGCAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCCAAGTTCCGGGCTTCTCTCAGTCTGGATGGCTGTGGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGJAGGGGCGAGGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGGTC AAGACCTAACTTCTGGA
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTCAATCAACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCTAAAT CCCTATTATTCCATGATATTTTCA/T/CJAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	CCTTTGCTCT AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAG	GGTGTCTTTCATGATTTTCTCATTTCCCTATCAGGTTTCTGGTCCCTTGTCCCTCAATTTTAAACATT T/CJCTTTTATATAGGGAATTAGCCCCTTAACTGTGGTACATGCTGCCAAAAATTTCTCCAGTT
WI-16406	24 C T	GCCTTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCCTTAATGGCTACAGAAAGAGG/C/JGGTTTATTCTTTTAAACACATCTGGTCTGGCAGC AAGTTATATTATGCAATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTTCATGATTTGTTTCATCTGAGAAATAAACTTCCTGCTAATTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGTGCTGAGCCAGCAACCCTCGAGTTACCGGCCCTTTTACCCACGGC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T C	---	---	AGAAACATCTGTCTGATCAGAGGAAGATGTATGTAGAAAATCAGAAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGAAAAGAAAATGTTTGCATAAAAGCTTTTCCCTGACTCTCA GAGGGTTTCAGA
EST39371 9	86 A G	CATTGGATTA GGGTGAGG TT	TGATTTGAGAC ATTTACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTAAATCCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCCTCAAATCAAATGCTTCTTCTTAAAGATTA GACATTGCCCAACCCTGC
WI-17177	23 A G	---	---	ACAAGTGACATATCCAAACCAAC[C/J]TCCATCCCACCTGTGCCCCATTCTTCCCTTGTTCTTT AGAGCCTTTTCAGCTATTTCCCTGTGAAGCAAACTGCACGAAGGCCCTCCCCGTACTCCTCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA TATTGATT	GGTCCCTTATG AAGCCACC	AGGTTCTCTGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCAAGGGACCCAGGATTCTGCAAT TTCTGGGTGGGCCCTAGGTAATTCGTTCCTTTGGTCCACAGAGACAAATTAAGAAAGATCAGGTCT GGCTGTGTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGT C	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATACCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA	TCCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAAATAACAGGAACCTATTATAT ACGTAAATCACTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAAT[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGTGG[C/J]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCCT GTAGACATCT	CAC TTGCAATT CTGAAGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTCTTGACCAAGCCTAAAGATTCTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C	---	---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTAAGAGTGTAAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACAGTITTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTTGTGAAAGTGTAAATGTGCGATG GCTATGTAGACATAAGA
EST40601 9	78 A G	GCGTGAACCT GAAACAC	TTCTTGAAGA AAGGGTC	TCCAGGATGGTTTATCCAAAGCTGTGACGGTGAACATTAAAGACGAAAGAGGTGACTCGCGTGGA ACCTGAACACAG/GIGACGCTTTCTCCAAAGAGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTCAGGAT	GCACACCCCTC ACACTGTTA	TCCATTCAAGTGTATCACATCTTCAGGATAGGTAG/GATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTCCCGAGAGTAGCAGTTTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGGA	AAAACGTGATT GTTAAAACATG CTAC	ATGTCATTCTGGTCTTATTTTGGACA/C/TGTAGCATGTTTTAACAAATCAGTTTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTACAAAATTTCTCATCTGTAATTC
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC	AAATCTCAGC ATTGCTATAAG C	AGAGAGACAACAAGAAGAAATAGGGGAAAATGGGAAGAACAGAGTGAATTTAAAGCAAATCTTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATTCGTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG	CCAAGATTGTC TTTAATTTTAC TC	AGAGAGACAACAAGAAGAAATAGGGGAAAATGGGAAGAA/C/TJAGAGTGAATTTAAAGCAAATCTT GGATTCAAGATTCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATTCGTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CAACCCTGTCT AGACAGATTTC	---	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCAATGCACACAACAACAGGAGGT/CJGGGGTGCACACGGGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	CACCTGTCT AGACAGATTTC	CCTCCTGTGT TGTGTGCA	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCA/CJTGACACAACAACAGGAGGTGGGGTGCACACGGGGAGAGCCAAAGAC TAGGGC
WI-18449	129 C T	CTTTTGGCTCT AAGTGGGACT	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACATAAAAAGGAAAGGAAGAAAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTTCCAGTTCCTTTTGGCTCTAAGTGGGACTA/C/TTC TGGATACAGTCAGGGGAG
WI-18457	120 T C	---	---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTCCCCCAAGACATTATTTTATTCCTT AAATGTCCAATATCGCTGATGTCTGTGTTTGTGCACATTGGGGCCACAGT/CJAAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGGTTCT	GGTGTATAGTGTCTGTACACCACAATGGCAGAGGTGA/GJTAGAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGTCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18476	60 C T	GGTGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGCTGAGGGTGGGGTGCAGAGG/C/TJGGT CACTCCCATCGTGCCCTGGCGCTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT

WI-18491	109	G A A A A A T G G T	A A C A A A T G G T	CGTGTGATTT	CTAATGAGATGAATACATGGAAGGGGTTTAGCACAGTGCCCTAAACACACAGTAAGTAACCAACAAT
EST50757		A A A T A C T A T T	AGGTGGTATT	TC TTGTAATCC	GGTAGGTGGTATTAATACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA
b	79	C T C T G C T C T	G A G C T C G A G G	ACCTTCACCC	OGT
				GGCC	AGCCCCCTCCACTCCACTCTGCTTCACAAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTTCTTTTATAT
WI-17675	103	T C A T G G T G A C T T	G G A C A T T T G G	GGGGAACCACC	GTGCAAGGGCC[C/T]GGGGGGTGAAGGGTCAGAGA
				CAGG	GATCTTGGAAAGCACTAGAAACTAGAAACTAAACATCTTACCAGGTGCTGAAGAAAAGTGCTTCGTTTTAAT
					TGCCAAGCAGGGATGGACATTTGGATGGTGACTT[C/T]CCTGGGTGGTCCCATAGATTCACCAT
					TGCCCTCTAATGGTGCTCA
					GATCCATTACCTAGGGTAAATCTCCTGAATGTCAAAACAAAGAGATAAACTACATTTGGGTTTGG
					G/TAAAGTCCCTGTAAATGAATCAAGAAATCCTCAAGTCTGCTTGCCACCCATTTAATACGTATT
WI-16543	67	G T T G G	C A T T T G G G T T	GATTCATCATTT	TTTGTAAAGGCTGAAGTT
				ACAGGGGACTT	ATCTGAGATGGAAGAGTTTCATCCCAAAACCCTGACCCCTGACCCCTGAGTCCATGGAAAAATTGTC
				TTACTTTTGTGTA	TTCCACAAAACCCGGTCCCTGGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTGGGTACAAAAAGTAATT
WI-17687	107	C G T T G G G A A	G C C A A A A A G G	CCGACCAGCA	G
WI-17690b	79	A G ...		---	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGGAGGCAATTTTCTAGCTGTGTTGATTT
WI-17690a	63	G A T A G C T G T G T T	A G G C A T T T T T C	CAAGAGTTATG	GGCTCCCTATAG[G]GATTCAGGACCCATAACTCTTGTTCTCACTATCTGCTATGCTGCTG
				GGTCTGAATC	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGGAGGCAATTTTCTAGCTGTGTT[G/A]
EST51717					TTTGGCTCCCTATAGATTCAGGACCCATAACTCTTGTTCTCACTATCTGCTATGCTGCTG
b	128	C T G T G A C T G T T	G C G G A A G A C A	TTGAGGCAATA	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTAT[C/T]TGAAGTGGAAACCCCTCCGACCC
				ATCCAGCTC	CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGAGCGGAAGACAGTGAGCTGTTCGAG
EST51717	39	C T ...		---	CTGGATTATGGCTCAAA
a					TTTCCAGGTTGACAGGTTTATCCACCCCTTCCATCCCCATGGCCACCCAGGAGGAGGAGACAG
					GTGTGCTGGAGTCTGTGCTACTTTGGGGC[C/T]GGCGTGGGAGAGCCCACTGGGTTTACATTCTCTGT
EST53012	97	C T G G G C C	T G G T C A C T T T G	GGCTCTGCCCA	GGGCAGGTGTGGACAC
				GGCC	
					AAACTGCAATAACAAAAACAAAGAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG
EST53349	96	A G T A C	A G T C A C A A T G	CATCTGGATAT	AAGTATATGTTGAAAGCAGTCAACATGTAC[G/AAAATGTGACAAAGATATCCAGATGTTTAA
				TT	TTTCCGAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCGAGAACT
					TAAACAC[G/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTTAACATGAAC
EST53389	74	A G C A	A G A A C T T A A A	CAATAAATGCT	ACATTAAAGGGGAGATGGCC
				C	

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TGR- A003P30	117	C G	---	---	ACAAATTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTCTCAGAAGCCCTGTGATTTCTCTAGGA AACCATCTGGGTTTAGCCCAATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TGR- A004S34	156	C T A	CCAAACCTCCT CATTCCTATAA	TGTAACACAGCT AACTGTTTTTG TTAAA	GCTTGCTTTTATGTTAGGTTGGGGGAAAGGAGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGGAGGTTGCAGAACCTCTTTGCTTGGCTAACAGTCTGTCTGACATAAGCCCA AACCTCCTCATTCCTATAAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACAIG
TGR- A004T44b	97	A C	---	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTTGATGGCGATT[C/G]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TGR- A004T44a	69	G A TGA	GGAAGATAAA CCAAAATGAT	GCCATGCAAAA TTCCTTATCA	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAAAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TGR- A004V08	60	T C	GAGGAAAACA GGCATCTCTT	TCCTCCCA AAGGC	CCTACAATCCTATAATATTGCAAGGTTGGGAAGGATGCAGGAACACAGGCATTCCTTAT[C/G]GCC TTTTGTTGGGAAGGATCAATTTGGTGCATGCACCTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TGR- A004V26	125	A G	---	---	TCTAGCTATAAGACCAGATTTTAATAATTCTAGATATAGAAATTCAGAAATTAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAAAATATGCATTATCTTCACATGA[G/G]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTTGCTTAAATACTGTATCTATTGG
TGR- A004V28 a	29	A G	TGTTGTGGGTG CGATCTC	CGGAGGTTGCA GTGAGC	CCAGGCTATAATGTTGGGTGGGATCTC[G/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCCTCAGCCCTCTTGAGTAGCCGGGACTACAGGCAACCCGCCACCTAACCTAAATTTTG TATTTTGTAGTAGACATTTGATTTTTTAGTAGACAGG
TGR- A004X20	25	T C G A	AAGTTTTCCCT CTCTCTGTAG	TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTTCCCTCTCTCTGTAGGA[C/G]GCTCCATGTTACAGTCAACTATAAACACATGGCTCATGT TCACCTCTGGGCTTCGGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCCTTTGTTCTGTGTCTTTCA GACCAACCCGCTCTCTTTCATTTCTTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATGTCCCAATC ATCATCATGTCCCT
TGR- A004X30	26	T C	TTTGAATCTT AGAGTAGAAC CCAC	TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAAATCTTAGAGTAGAACCCAC[C/G]ACTCTAGTAATACTTGTAAATAAAATTAATAAGTTTT AAACACTTCCATAAAGAAATTAGGGTGCCAGCTCCTTGATTTCCCTAGGGATAAAGATATCCAT GTTAGGATAAAGATATCCATGTAC
TGR- A004Z04	102	T G	TTCAATTTGGGT ATGCAAAACT	CTTATAATTAG AAATTCATGA AAGCA	CACGGTATATGCCCTTATATATAGGTATATATACAGATCGTACACAATATATTAACAGTTTGACATG GGGTCACAGTACCTTCATTTGGGTATGCAAAAC[C/T]GTTGCTTTCATGAAATTTCTAATTATAAGG ACTGTTGCTTCTTCATATTCATTTCAATGGACATTAACAAAAATACAGTCTCTTTAGTGAATTAAGACGTC TCTTAGTGATTTAAGACTG

-221-

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTTC/CTCTCCGATGACCATCTTTGGGCTGGGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT TAGGAGACT	CAGGGCTGCCG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCAAGGGCCAGGTAGCCTTCAGGGGGGGCA GGGTTGGGGAGGTAGGAGACTCTGGACCCGGCAGCCCTGGCTCCAGCTTCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C		---	TATGGAAGTGTAGAAATAATGATTGGACAAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGGAAGGTCTGCTAGATTCTCTTGGCCTCTCTGTCAGGATTCCTTCTTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGAAGTGTAGAAATAATGATTGGACAAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGGAAGGTCTGCTAGATTCTCTTGGCCTCTCTGTCAGGATTCCTTCTTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D44	97 G T	TTAACATTAT GAACCTTAAA CTGTACAC	TTGTCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACACAAATGGTCATCAACTGAACCTTGGCTCCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAACTGTACACTGTG/TTTTTGGCTTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTATTACTTTGTAGACAAAGTATTACTTTGTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACAGGCTCTG/ACTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACTGCCCTGCCATGTGGATAGTACTCTTGGCTGCTTGGCCCTACAAAGCCACTTCTAT TTTATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	AGTAAGGTTA CTGCACCTTAC	---	CTCAGTGTAACAACTTTGTTAGGGAAAAAATAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGCTGAGACAGAAATGACCCCTTGGGCTCCTTTATTTTGTCTTTTCAACAGGACC CCACAGATATTTGGGTATGTCATGAGGACTGGGATGCTCTTATTTG/CJGGATGCTCTTCTATTTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC	AGTAAGGTTA CTGCACCTTAC	GCTGAGTTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAG/AG/CTCAATTTCCCTGATTTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGAAGTATAAAATGTTGTATTTAAGAGAAATCCCAACAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGCTAAGCACCTACTGGGTATCAGGCACCTGACTCGG TGCTTTAC/AG/ITACATTACCTCACAGCCAGGGTTGGCAAAATGGTCAATTTTGACAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CT/GCTTAGGGTGTCTCCCAACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGACACTTTGTCTGCTTACAGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCTCTTGATATTGTAAAAATTCOCCCAAGAGCGCATATGAATCTGCC

-222-

X57830	106	G C C T	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCACGATCATATCTGTCATGCCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGGAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G T G G A T C	CTTTTAAAGAA ATTTTGTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATGACTGCTTTTAAAGAAATTTTGTATTG GATCTTGGATAAATCTAGATCTTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTGTCTTATACACAATTCATTCTTTCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T ---	---	---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACCAAGCTTGTAGAGCTTCTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACGCTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAGTAAGTGAAGG TCCA
D28513b	133	A G ---	---	---	ATGACCAAGCCACCACATTTAGAACCTTTGGCTGGCTTTGGAAGTCCAGAGCTGGATCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAAGCAGTTTGTATTGACTGCATGAATGC[A G]GTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAAGTTCTGCTTC AGCTGTACATA
D29833b	85	A G ---	---	---	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTTCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAA[A/G]TTCCTCAACTGATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D29833a	21	A G ---	---	---	CCACTCCATCCTGATGCCCA[A/G]GTTATCCACAGCCTCCTTCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACTGATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAAAGACACCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D31762	82	G A ---	---	---	CTCCCTGCCTCCTCCTTCCCTGCTGCTGATGCTCCGCTCTCAACACAGCCGAAACCTGTCTTGCAATGGGG GAGGGGGCGTTT[G/A]CTTTCCCTTCTTGGCTTCCCTTATTCCTCACAAACCAATTCCTCAATAAA GCCAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGTCTCCTCACTCCTGTCTGCTGGCTTTT CTGGA
D37931	64	T C ---	---	---	ATTATCGCGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG[T/C] CCCAGGCTCTGTCTCCTCAGCTCATTTCCCTACTCTTTTCTCTATATAACTCATTTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTATGAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT

D63807	101 C T ---	---	---	CAGCAGGACTTCAGTGTGAGTATCCCTGCCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTCTGTGTCAC/C/TGAGAGGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTCTGTTCTCCCTCCCGTCGGCTTCTCGGTGCTGGAGGGTGACCTGCTCCAGATGAC
D90145	21 T C ---	---	---	TGGGAACATGCGTGTGACCTC/T/CJACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACCTAAATTTTAAATTTATTTATATACTATTAGTTTATTAATTTATTTTGAT TTCACAGTGTGTTTGTGATTGTTTGTCTGTGAGAGTCCCTCCCTGTCCTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035	59 T C ---	---	---	ATTATCACTCTCAAAAATTTGGTGTGTGTGTTTAAAGTACTTTCTTATTTATGAGCCCTT/C/JGAGGA CCAGACATGTTATTATCAAGCCCTTATATACCATCTAAT
EST16668	71 C T ---	---	---	GCATTTTAAATTCACATTGAATCATTATTACTATTATGATGTTTACATAACAATTCAGTATCATTT ATG/C/TJGTAGATTCAGATGTAGTGTCTCAATACGTGACCTTATCT
EST16904	57 C T ---	---	---	ACAGACTATCGCCAACCTTATAATGCTTAAACTTTTATGATCAATAGTAATAATTACA/C/TJGAGATA TTCACACCTTATTATAAAATAGGGTTTGTGTAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863	49 A G ---	---	---	TTTTAAGTACCAGAGGCACTGTCTGGAACAGGATGAAAACGTGATACACC/A/GJTTACTACTTACTC TTCACCTTCAAACTGATTCCTTAAAGACTTCTACTTAGCAAA
EST21885	80 G A ---	---	---	GGCTGAAGTAGAATCAAAAGTTAAGAACATTTTATGCACTTATCCACAAACATTTACTGAGCATA CTAGGTGCTGGG/A/JTGTGACAGTGAGCAAAAACACAA
EST22623	26 A G ---	---	---	ATTTAGTGCAATGACAAAGCCCAA/A/GJAGAACAGAGGATCAAATAAGATTGAAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACAAAGTATGGAGT
EST22644	98 A G ---	---	---	AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/A/GJAAATGTGAAAAGATGGCTTTTAAACCC
EST23587	31 T A ---	---	---	CCTCATTTATTTAAAAGACGGACATAAAAAA/T/AJATACAACAAAAAACCCCAAGTCACATTTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST24246	106 T C ---	---	---	AAAGATCTGGCATTATTCACATCATCTAAATATTTTGTAAATCTTTTCCATGAGTATTTTTC TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/T/CJGAATAACCCATAGTTACAGAAATTGG GTCTGTGAACCTCAATT
EST24308	45 A G ---	---	---	TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/A/GJCATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435	73 G A ---	---	---	CTTGAACTTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/G/ATGGCTGACCCACATTTCTTTATCCGATCTGTGTGATGGACATTCAGGTTGTTTC
EST25089	25 T C ---	---	---	TATTGTTGCATTATCAAAATGGTTA/T/CJAGTTTCAATTAACAACTGTAATTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAAATGTAGTTTCCCAATCGTTAGTTAATGCTACATT

EST25476 9	33 G A ---	---	AATGATCTTTATTTCAGACCTGCTCCTAAAA[G/A]CTTTTCTCCTCCTCTAAAAAACCAAAACACA AGAGGTCTCTTGCTGCCCTTCCATGGACTGTGGCGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---	---	AGATAATGCATTAGAGCCTGCCCTCATTTGTATCTTGATTAACCTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATTCCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---	---	AGAAAAAAGGTGCTACCAGAACTCATGT[C/G]ATAGCGCTTCTTTAGGCACATATTATAGCAATT CAGATGAAAGTTCTGTATACACACACACTGTGCCICTAACACAAACACGGTGACTCTGA
EST27816 5a	26 T C ---	---	CAACTCAAGGTACAAGACAATTGCATT[C/T]TAACATTGTTATAATAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCAATGTT
EST28588 0	78 A T ---	---	GTTTAATTGGGTATGGTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCCAAAAGAGAGAGGAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 A C ---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAECTTAECTTTCTTGA AGGGAATATAAACTACTGAACAAGACAGACTGTGTAACTTAAACAAGACAGACTCATTTCTCTTTGA G
EST30935 9a	59 C G ---	---	AGCTATGGTAGAGCAAAATCCAGTGGTGAATAACAAGAACTCTAAAGTTCAGTAGAGA[C/G]JAGGT GTTTTGAATGTCAAAGGAAATCACTGAGGTAGATTTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCCTCTAAACCTGTTGAATAGAAATATGGCCAAAT ATTACAGTTTCTCAGTTTCTCTATGAATACTGGCAGCTGTTTATTTCAATGTTTATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	TGCTTTGTTTCCCTCCAAATCCTAAAA[T/C]GTGTGTCTTCAAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGTACCATATTTCAAGTATCTTGAATACAGGTTTCAGATACTATGGAGATGATACCACT GGACTAGGTA
EST33352 7b	75 C G ---	---	TACACATTATTCAGAGACCACCTGACATGCATCTCCTCCGAGAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTTACTAAGAGAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 A C ---	---	ATTTTCCCACAGCAGAAGTATATTTATGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACGAGTACAGAATGTTCACAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C/JAAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 A G ---	---	CCTTTGGGGGAGTTTTAAGCCAGAATGTACAAAAGTCACTTACAGGAAGACTGGAAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---	---	AAAAACATGCTATTTGAACAAACTTTTTTATAAAGAATAAGTTG[A/C/T]TGAAAAGCAGTTTTTAAAT AACATCAACTCAAAATGACTTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---	---	AAAAACATGCTATTTGAACAAAACCTTTTATATAAGAA[A/G]TAAGTTGACTGAAAAGCAGTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	ACAAATAGGACTGGTTATCTTGGTTTGAATAATATGTTGCCACITCCTATTGTTTTAAAAATGA TCATTTAAC[C/T]CTTTGAACACAGCCTGAATCCCCC
EST34739 3	97 T A ---	---	GAAATATCCTTCCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTC[T/A]GGTGCTTACAACTCCAACACTACTGCAGAAATTTCT TGTTGTGCCTCATAAACA
EST34792 6b	104 A G ---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCAGATCACTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTAATCAGGAATCTTAGTCCTATTACA AAGATTTTGTGCTGTG
EST34835 9b	93 T G ---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGTGCTTCTGG[T/G]GGCCTTAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTT[G/A]TGCTTTCTGGTGGCCTTAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST35230 0	93 G T --	---	CACAAAGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCACTCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAAACCT
EST35337 9	33 C T ---	---	TCCTTTCAAAATTTTGTATGATGAGCATTTAATG[C/T]ATAAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTTTCCATTTTACTTAGTTCAGAACCTTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	CTGCCCCAAATTAACCTTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCTCTGTTGTG ATGTCAAGTGTGGCT
EST35747 9	51 C G ---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---	---	TGGTCCATTATATTAACCTGAGGGAAACAAACGGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCCTCCCATGAAACCAAGA[C/A]CTTGTCTCATGATAAAGTGGAGACAATAAGAAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93 C T ---	---	CACCTGTTTCATTGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCACGCTACAGC AGTCAGGAGGCGAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---	---	GCCATCAGCCCCACAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATCTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGTCTTAGTCGT

-226-

EST36620 6	50 G A ---	---	GAC TTATTAGATAAGGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAAGACTTT
EST36690 0a	89 C G ---	---	CCGTGATGTGCATGGGTGCTGAGCAGTCGTACTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGGATTCTCTA[C/G]AGGGGACATATCACACATATTTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	GAGACAGAAGCCATCAGTTAAATGAGGTAGGCTCTCCTCCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAAATACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGGTGCTATTCAAGCAACAAT[AT/TT]CTTTTATGTTCCCTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTCACTCTCTTGCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACCTGGTCC TTGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGCTACGGGCCCCGGGATGTTAAAAATTTGGGATTTTAAATTAAGATTGTGAACATG CAAAACCCAGCAATTTCTCAGCTTATATTTGAAAGTCT[T/G]CAGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAAGACCTTCTCAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACCTCTAGGAA[G/T]AGTAAACAGGTGTTAAAAACCTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACATAAGATATCCTCTCCTCAGCCTCCACAGTAGT TGGAACCTATAGTAGGAGTATC[T/A]G]CCCTGCCCTGCTAGAAC TTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACCTT[C/T]AAGGGTGAAAAAGCATACC ATTCCATTTAGTTGAAATATTCCTTCACATAGCCCAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGTGTAGCGCTGGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTGTGCTCTGCA[G/C]GCTGTCTCCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGT[C/T]GAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTGCTCTGAGGCTGTCTCCTCAGGCAAGTTGCTGACTTCTCTGT GTCAGG

EST37378 9	63 T G ---	---	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCGTGAAAAAC[T/G JAACATGCCTCAAAAAAGAGGGGAAAAAACCTTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---	---	AAGACATAAATCTGCAATGAATCAGTTATGAATATTAAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTAICGCACTTTTAAACACCCCTTAAATCAATGACGTAGAA
EST37613 6	34 A G ---	---	CTAGGCATGGGGCTTTTACAGTCAATTTATTTACC[A/G]GTCATGAATTCATTAAAAACACAGCGAT ATAGCAATGAGCAAAACAGACCCTCCCCAAATACCCCTGGTTCATGGATCTTCCATTCTAA
EST38025 4	56 T G ---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATACCTTAT[G/T]TATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---	---	TCTACCAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACCTT[A/C]TCGCATGG AAGAACGCTCTCCTTTTAAATCCCTAACTCCTCTCTCTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---	---	TAAATCAAGGCTCTTTTCATTACCAAAACAAAAACAAAAAAGGGAACAAAAATACGATGGAGAGG GAAGAGATGATGCCGAAGTGTCTATCCTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C ---	---	TTTATTTGCAAAAGTAAGCAGCCGG[T/C]TGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGACTTACATTTGACACAGGCTAAAAAGTATGGGATGAGAGAGGAACAAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---	---	TTTTTGTACTCTGTAGCCAGTCATTAACTGAAGGTTTAAATATATATATATTTATTGGGATGAGATCA TAGTCTTTACACAAATGCTATG[T/C]AAACAAAGTTACTGAATATTTTACCTCTGGAGTTG
EST39331 1	70 G C ---	---	TCCTTCTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TG[C/G]GTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTGGATACATCACT
EST40544 7	31 C A ---	---	GTCAACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACITTTATCACATTAGCTAICGAAGTTTGAAATTT
EST40548 4	37 T C ---	---	TTCTAATAGCATGCCCTGTGACAGGGAACTAAGCT[C/T]CTCAAAATAACTGAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCCTTTGTAGTTTTTCTCCAGAAGGCTCAAGGTGTTT AATAATCTGTGGGACTCA
EST40549 1	42 A G ---	---	TGTTTCTCTAGAGAACCCTGTGTGATACACTACGCATGCACA[AG]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACATTTCTCACITTTGAACCTAGCTCCCTGCAAAGCACCTTCTA CCCTGCACITTTGGGGAG
EST40579 1	81 A C ---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTCACTCTTACCTTAAAGTCTGTCTATCTG AGCTGGTGGAAA[A/C]GGACTTGGAGACAGCGATTTAAATACGGAACAAGGTCTTCCAGGAAG
EST40584 3	68 A G ---	---	TTGTATGGTTGTAGGAATTTGGGAAGAAATTTATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A[A/G]TCTGTACTCCCAATATCCTATGTTTAAAGCT

-228-

EST51340	51 G A ---	---	GATCAAACTGTATTGCCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCCAAGGATTATT
J04162	134 T C ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTCGAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA[T/C]TTTCCCTTGGTCTCCAGTGGAAAGGGAAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	CTGAACCCAGCTGCCCTACAACTCCAATCTCAGCTTTTCTCAGCTTCATGTGAAAACACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTTCCAACAAATAGAAATTAAATGACACTTTGGTAGCACTAATATGGAGATTATCCCTTC ATTGAGCCTTTTATCCT
L18877	69 T C ---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGAGGGAGTCTGGCCAGTGCACCTTCCAAGGCC CT[C/A]TCCATTAGTTCCACTGCCTCGTGTGACATGAGGCCCATCTTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTCTGTTCTATTGGATGACTTTGAGATTATCTTTGTTTCCCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	GCATTTTACATATCCCAAGCCCTTTAGGGCTACAGT[C/C]CTTTGCTCTGGACCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAAGAAAGGCTTTGGCCCTGGTGTGGCATAGGCCTGTAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGGCAACACCGAGCTCCCCAC CC[G/C]CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTATTCTTTTGTATTTTGTATATTT[G/CGCCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGTGGGCTGTGTTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	CAAAGTTGCTCCTGCCCATGAGCACACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTTCTCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

-229-

L48728b	111 T C ---	---	---	AAAGTGAACAGAAAGCAAGATGGATTGTTCCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAAGAGAGCTCAAGTTTTTGGTTACTTTTCAGAAATTC/CJGAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	---	GGCACAGTCCAAAATACAAATGGACAGAAAGATCTATATTGTACCAGAACT[G/A]TTTATTTTCACC CCATCAAGTATAAGGTTACTGATTGATGGTCCCTTTTATAAACATTTGGTATATTTCCCATTCATGCCAA AGCAAAAGAAATAAAAGCTAA
M19169	113 T C ---	---	---	TAGGGATCTGTGCCAGGCCATTGGCACAGCCACCACTCCACCCCTGTAGTGTCTCCACCC TGGACTGGTGGCCCCCACCCTCGGGGAGGCCCTCCCATGTGCTGTC/CJGCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCCTTTGTGCTCAGCAGGGCGCTCCGCCCTCCCTTCCCTTCGCTTCTAATA GC
M21539	114 T G ---	---	---	TCACCTCGTTCACAGCTCCACCTGCATCTTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCCGACAGCAAAAT/GJGTTTTCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCCCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTTGGGTGC
M26041c	173 A G ---	---	---	CCTAGCATTATTTCTGGCCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCTCCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCTTTGAATTTATTTCCCTGACTTC CTGATTTTTTCTTTCTCAAGTGTACCTACTAAG[G/A]GATGCCTGGAGTAAGCCACCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	---	CCTAGCATTATTTCTGGCCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCTCCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCTTTGAATTTATTTCCCTGACTTC CTGATTTTTTCTTTCTCA[G/A]G/GTGTACCTACTAAGAGATGCCTGGAGTAAGCCACCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	---	CCTAGCATTATTTCTGGCCCCCATTTATCATATCCCTTTTCTCCTTTCTCCTCTCTCACC TCTCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCTTTGAATTTATTTCCCTGAC TTCCTGATTTTTTCTTTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAGCCACCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	---	TAAGGAGCTGTGAGGGAGGCCAGTCACAGTCCAGCAATCCACAACCCTTGAC[G/C]AATGCT TGCCAAAGCTGTTTTAAAGCCCAAGAACACCCCTTTCTTTGTTCCAAATTAACCTTTAGAAGAAACCCCA CAATAAAGCAATCAATC
M81695	34 G A ---	---	---	ACTTACTTACCCTCACCTGTGAGGCTGACGGGA[G/A]GAACCACTGCACCACCGAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGCTTGTCTGGGAGGGGCTTTGTCTTGTCAAGGTTT CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCCAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166 C T ---	---	CTCCTCCTTTATTTAGCATGGAGGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAAAGATCTTTTCAAACTTACCTTGTAAAGACAAATTT TATTTCCAGGCTATTTAAATACGTACTTTAG[C/T]JGGAAATTTATCTATGTCAATGATTTTTAAGCTA TGAAATACAAATGGGGGA
U09607	39 T C ---	---	GAGGCTTATGAGGTCCTTACTTCAGGAACACCCCAT/CJGACATTGCATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTGCATTTTGAAGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTGTAGTCTGTGGCCCAAAGAGCAAGGAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[C/J]ACATCTGCCCGCCCTTCCAGCCCTTCCAGCCCTTCCAGCCCTTCTCTTCTTCTTC ATTCAATCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATTTCTT[C/G]GCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTGGTTCTTGTCTATTTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAATGTCTTTTAAATGGTCAGTTTAAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAAGGACTCTGGTTCAAAATCCAGGTTCCATTTTGTCTATCTTTGTGACCTTTCACAAGTTGTTTAAAC CTCTTTGTTTCAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCCAAGAGAT[C/J]TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGTCCACTTTCACCTGGTTTTTAATAGCCAGCCAGTCATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTTGGAAAGATTTAAATAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C/J]TGGTCTCATAC CTCATATGCAGGATTCAATCA
U17077	122 T C ---	---	TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAAACGGAAGATCCACT AAAACGTCCACGGGATTAACAGAACGTCCTTGCAGACTGAGCGATGACACCACAC[C/J]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAAAACAACCTGTCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAAATAGACTCAGCCTATGTCTCTGATTCAGCTGGGTAGTTCTAGAACTTT[C/J]AGAAG CTCCATCTTTTAAATGTTTTTATTTGTTATGTCCCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAAATAGGACACACGATGGTGTAGCTGAAGTTTGTAGCAATTAGGCACCTTCC AAGGCTTTAGTAGAGAGAGCC

-231-

U25975b	164 C A ---	---	---	TCACCTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143 C G ---	---	---	TCACCTGCTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61 A G ---	---	---	CAGGGAGAGGTTATTACAAACCTCACAAACTAGTATCATTTTAGGGGTGTGACACACCA[AVG]TT TTGAGTGTACTGTGCTGGTTTGGTTTAAAGTAGTCTCTATTTTCTATCCCTTAAAGAAAATT GCATGAACTAGGCTTCTGTATCAATATCCCAACATTCTGCAATGGCAGCATTCACCAACAAAA TOC
U28413	29 C T ---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTTCCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89 A G ---	---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATCCCACGTTAGCCA[AVG]TTGTTCTTGATGAATCTATAGTCAAGACACAAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCACACAGTTGAACACAAGT GCTGTCA
U30884a	34 A G ---	---	---	TAGGGTAGCATTTAAGATTCAGGAGTCATTAGC[AVG]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCACGTTAGCCAATTGTTCTTGATGAATCTATAGTCAAGACACAAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCACACAGTTGAACACAAGT GCTGTCA
U31216b	78 A G ---	---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTCA[CA/AVG]CCCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCAGCCGATTGCGCTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A ---	---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC[G/AVG]TCATAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGACCAAGACCCCTTACACGTAGAGGAGGAGGATGCCAGCCGATTGCGCTTAGCCCGCC TGGTAGCCCTTCCAT

-232-

U31416c	76 G A ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTGCTTACAATGTCTAGGTCCTCCCACTGCCTGCT GGAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---	---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCACGCCACAAATCTGGTGCCTCTCTCTGCTTACAAATGTCTAGGTCCTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---	---	---	ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCACTCACATTGTTCCCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGTTGCTGGAGCTGTACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTCTCTATCTGGGGAGCGCTCGAGAGAGCCGAGAGGCCCGCAGAAC ATGCCAGGTGTCC
U37690	54 A G ---	---	---	GACCACGCTGAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[G/G]CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ---	---	---	TGAACCGTTTCAACATGGAATGATCTGATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCTATAACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAGGAAACATCATGTTTACCTGTGCAGGCACTAGTCCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---	---	---	TCAAGAAGGTGACTGCCCTTGATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTTAAAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCCAGTAGCTAAGACCCCTAGAATTTGGATTCACTCTCTGTTTTTTCATGTCTCTCCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ---	---	---	AGGAAGATCCCACCCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTACATTAGGA ACCCAGACCGGAAAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAAGTTGCGAAAAATTGCG AAATCTGTTGTGCA[C/T]GCTCAAATGAAAACGCCCTTCGGCTTTGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A C ---	---	---	AGGAAGATCCCACCCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTCACATTACATTACATTAGGA ACCCAGACCGGAAAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAA[A/C]GTTGCGAAAAAT GCGAAATCTGTTGTGCACGCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTATTTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

-233-

X54741	24 A G ---	---	CAGGCCACCTGTCTCTCTCCAC[AG]TGACAGCTTCTGAGTCAACCCCTCTGTCCAGCCAGCTCCTGGACAAATGGAAGTCCCGAGGGCTCCAGGACTGGGGCTTGCCAGGCTTGCAATAGCAAGGCCAGGGACAGCTGGAGACGATCTTGCTGGCAGGGCTGGCCTTGTCGCCAGCCCAACCTGGCCCCCTTCTOCAGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTTCGTTTACAGTGCATCAGATACATTTTATTTCTTAAATAGAAATATTATGATTGCATAAATCTGAAATGAAATGAAATTTGCTCT[AG]ATACAAAATCTAAATCAATTAATTGAAATAGGATGCACACAATTACTAAAGTACAGACATCCTAGCATTTGTGGGGCTCATTTTGTCTCAACATGGTACGCGTCTGACACCTCCAGAACGCAGGTGCTGGGCCCTTCTGCCTGGGACCCCGGGAACCTCTCTGCCCGAAGCCGAGCGGATGGGCCCAACTTCGCCCTGCCACTTGACTTCACCAATCCCTTCCTGGAGACT[GA]AACCTGGTGTCTCAGGAGCGAAGGACTGTGAACCTTGCGCTGAAGAGCCAGA
X66924	147 G A ---	---	GAAATGTGAAGAAATGTGACAAAGCCTTAAAGCGGTTGTACACTTGATTGTATATAAGATAA[TTG]TCACTGGAGAAAACCTCCAGAAAGTGTGACAAATGTGACAAAACATTTAAATTAATCTCATACCTTATTGCACAGGAAAGCATTTATACTTGAGAAAAATTTGTATAAGAAATGGAAGATCATTAAATATCTGCTCATATCTTAACATCAGCGAGTT
X78932	62 T G ---	---	CTCAACCCATAACCTCAACCCACATCT[CT]ATCTCTCCACCCACATCCCACCACATCCACCTCCATCCCAACCCATCTCATCCCCAACTACAGCCCCAACCCAGCCCCAGACTAATCCACAGCCATCCCCAACTCATCTCATCCCCAACTGCAGCCCCAACCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAGCCAACTCAACACCATCC
X80026	25 T C ---	---	ACCCAACTCAAGTCCAGGCCCCAGGCATCTTCTGCCCCCTGCCTTGCTTGGCCCCATCCAGTCCAGGCGCTGGAGCAAGTGCCTCAGTACTTCTCTCTG[CTG]CACTTTGAAAGACCCCTCCCACTCCTGGCCTCACTTCTCTGTGTATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAGACCCCAACTCAAGTCCAGGCCCCAGGC[AG]TCTTCTCTGCCCTGCCTTGCTTGGCCCCATCCAGTCCAGGCGCTGGAGCAAGTGCCTCAGTACTTCTCTCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCTCACTTCTCTGTGTATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAGGGACCCAGAGTGACCAAGTCCAGCAGGAGGGCGCGCTCGCCGTGTCOGTGTCTTTCTTTTCAGCCCCGGAGAGGTCTGACCTGGGGCTTCTCAAGCCTCACTGCGCCACGCTCCCGCGCGCTCTCTTTCTCCCAAGC[GA]AAACCAATGCGCCCCCTTCACTGCGTGCCCCGTGCGAGGCCGGGGCTTCTTTCAGAGC
X80197a	28 A G ---	---	ACCAACAGCCATGGTCTAAGGACATGGATGGGTGCCCCACAGAGTGTGACAGGGGACCCCTCTGCCC
X85106	150 G A ---	---	CAGCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT[GT]GGGATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACCTGTCCAGGCTGAGATAAATCCC
X87160	128 T G ---	---	GGGA

X87344	34 C T ---	---	CATCCAAAGGCACTGGTGGTGACTCTGCTTCTGTC/GTACTGACCCAGAGCCTTGCTGTGCACTGC AAGCTGTGCTACTCAGGCCCAAGGGGACTCTCTGTTCCATTCTCCCCACAGACCTGTCAAGAG AAGCATGACAAACAAATCATTTACCGACTTTAGTGCTTTTT
X87838	179 G T ---	---	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCTATGGGAACAATTGA AGTAAACTTTTGTCTGTGCTCTTTTGGTCGAGGAGTAAATACAAATGGATTTTGGGAGTGACTC AAGAAGTGAAGAATGCACAAGAATGGATCACAAGATGGAATTA[G/T]CAAAACCCTAGCCCTTGCTT GTAAAAAT
Z14138	81 A G ---	---	GTCTGCTGCCTCTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTTGAAGGAGCAGCAGTGTGA CCTCCTGTGACCC[G/T]GAATGTGCTCCAGCGGCCCTGTGTTTGACATGTGAAGCTATTTTGAT ATGCACCAGGTCTCAAGGTCTCATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTCACA GAAGGAT
Z18859	191 A C ---	---	TAATCCTCACCATTCCTCAGGTATAAGTTCTATAAACAGGCTTGGATCTGGTAAATTAACACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC[A/C]CAGGTTT CAGTACTGGTTTCCAA
Z23091	159 G A ---	---	AGAACCTGACCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGCTGCTTGTCTCTCCCTCCCTCCC CACTCCTCCTCTCTCTCTCTCTCTCACTGCCAGCCCTTCTTCCCTCCTCCTCCCTCCTCCCG CTCTGTGCTCTTCATTCTCA[G/A]GGCCCGCAACCCCTCCTCTCTCTGTCCCGCCGCTCTCTGGAAA CTGAGCTTGACGTTTG
11595b	125 A G ---	---	GTGGCATTGTTAGTAAACCTTCATAGGTGAAGGAGGAGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGTTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTCTACCTTGCTTTGTGTTGAAGGAGTGGTTCCCATGACTGTTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCTTGGCTTGGAC
11595	125 A G ---	---	GTGGCATTGTTAGTAAACCTTCATAGGTGAAGGAGGAGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGTTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTGCTCCAGGACCTA[A/G]GCGTGC TCACTCTACCTTGCTTTGTGTTGAAGGAGTGGTTCCCATGACTGTTTAAGTGACAAGTGCCATGG ATATCTACACCGTCACCAGACTAGATTGTCTCAATGTCTTGGCTTGGAC
1241	131 G T ---	---	TATATCACATTAGTATGTCACCTGCCATGGTAAAGGACTTTGATCAGTAAAGGAAATGAACACCTTTGAA TGGCTTGCTCCTTTCAATAAAAGAGTGACATGATTGAACATGTTTATAGATAAAGGGCAGCTT[G/T]GCAGGAGTGTTTAGGATGAAGAGAGAGAGATTAAAGGAATCAGGAAGAAAAGTAGCAATGGGA ATGAAAATAGGAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAAG

1282	130	C T	---			GTGCGATCACCACACAGTCTAATTCAGATGTTTTTACATACCCCTAAAGAAATCTTGACCCATTA GCAATTTATTCCTCATTCCTGCCCTCACCCCGAGCCCTACTCTTTATGCTATAGATTGGCC[C/T]ACT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACCTGAGAATA ATGTTTTCAAGGT
6810	68	C T	---			AGTATCACACATACATAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTT A[C/T]AGAAGCATTTTTAATTTACAACACAAGCTCAAACGACCTACAATAAGTCTAGTAGTCTG TTTACGTGCCAAGGATAAGGCTGAACAATAAATAACCCCTTAAAAATGCTATGAACAAGTACAA TTTTCTTTTTGAGTTCTGCAGAGCAATGACCACATAAGAAATATTTTAAAGGC
6817	118	A C	---			CCAAGTACATTGGGTGAACGATGAGTAGTGTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGTAAC[A/C]GTGGATACCCCTG TGTGCTACTGGCTCCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGCGGCTGTGCAGATCGGCTTTTGGTTGGTGTAG
6819b	212	C	---			CCATTTTATTTTCTCTAAATTTTAAATAGAAAGACTTTTAAATGGAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166	G T	---			CCATTTTATTTTCTCTAAATTTTAAATAGAAAGACTTTTAAATGGAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
681xx	39	A G	---			CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTATACTATGGCACCATTGCGGACA CAGATTATATATGTCAGACACCACCGAATGTCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGT TTAACAAAAGAAATGAACGTCTAGG
6972b	149	G T	---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTTCAGAAGGAATGGTACCAGTTCCTCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTTGGTAACTATTGATTATTGG CACAAATTCAGA[G/T]CCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122	A G	---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTTCAGAAGGAATGGTACCAGTTCCTCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTAA TTGCCACAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACGATTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]GCTAACGATTTTACCTTGAGAAATGAAAATTATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA

-237-

7598c	56 A G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA/A/GJAGGAAC TCAATGAAATAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACAC/A/GJCCAAAGCCAAAGGAAC TCAATGAAATAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAAATCAAAGTCCCTCTATAAATT/A/GJTGATTTACAAAAGACACCCAAAGCCAAGGAAC TCAATGAAATAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCCTATTACAGACATCTTGCCAGCTCTCCCTGTA ATACTTTAAATGAATGGGTAGTCTCTATCTCAAGGTCCCAATA/A/TJCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCCTATTACAGACATCTTGCCAGCTCTCCCTGTA ATACTTTAAATGAATGGGTAGTCTCTA/JCTTCTCAAGGTCCCAATAAACCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCCCTATTACAGACATCTTGCCAGCTCTCCCTGTA ATACTTTAAATGAATGGGTAGTCTCTATCTTCAAGGTCCCAATAAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAAATGGGTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCC/A/GJCAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCATTTTTTGGCATTGTTAATCACTGAATC TGGGTTTTCTCTGAAATCCACACAGAGCATGCACACACAACTTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA/C/TJGGTCAATCCGAATCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG/A/GJCGCAAAATCCACTTTGCTGTAAACGGTCAATCCGAATCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATCTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8498	84 C T ---	---	AGGTTTCAGGGTTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG/C/TJAAATCTTCAATTAATCGAAAAAGAAAAAATTTGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGTCTTTAAATAAAAGGAGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCTCAATACAGAACCCAGGAATGTAATTTTCCCTAACTCAG

WI-18562	29 G A ---	---	CTAAGGAAAAATTTAATGATGGAAATATC[G/A]ACAAATATTTCAACATCATTTAAAAACAAAGTAG CTTCTCTTATTTACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTACAATGATTTTACATTTACATTT TAGCATTAAATCAGAAACGA
WI-18618	51 A C ---	---	ATAGCAGACTTTTAATCAATGCCAGAGACAAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCCTTCGATGCAAGTATAATTTGTAACACACAGTGTCTGCACACAGTTC AC
WI-18683	22 C T ---	---	TAAAGCTGTTCAGGACTGGACTC[G/TTGGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75 G A ---	---	GACTTTGGTGATTAAATGCTTTTCCCTTAAATATGAGAAATAGTGTAATTTCTCCTTTTGTCTTTT ACTAC[A/G]ACCGAGTGGTAAATACTACCTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCTCTCCGTGAGAC
WI-18563	94 A G ---	---	AAATAAGTTTTATTGGCACACAGCCAAAGCCCACTGGATGACACATTTGCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACATAATGTGAC[A/G]ACATGGTGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69 T A ---	---	GTCCTATTTCAATTTAGCTAGACCCATTTCACTCTGTTTAAATGGCTACATTTTGTTTTCATTGTGAGAC TT[A/G]TGCCATAATTTAATCACTGATGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94 G A ---	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTGTAGATTTTGTAAAG TGGTAACAGGTACATAGGTAACCAA[A/G]ATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71 T C ---	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTGTAGATTTTGTAAAG TGGT[C/A]ACAGGTACATAGGTAACCAAAGTATAGTTCTCATCCACATTTGACTGTGTAGATTTTGTAAAG
WI-18723c	96 A G ---	---	AACTTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTGTAGATTTTGTAAAG TGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44 G A ---	---	TTTATTACAATATTTAGGTGGCACAAATAACTAACAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76 G A ---	---	TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGCAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTAAATAAAAAATAA TGGAGCTACAACCCACCC
WI-18535	107 G A ---	---	GTAATAAAGTTTTATTGGCACAGCCACGCTCGTTTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGGTCCCCCGTG
D17525	107 C T ---	---	AGAGTGGTCAGAACACACAGCCGAATCCAGGCTCTATCACTTAGTTTTCAGTTCTGGGCAGGTGAC TTCATCTCTTCGAACCTTCAGTTTCTTCATAAGATGGA[A/C]TGCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATAACACTGTTT TCAATAATGCACCTTAGCAGAAGGTGATGTCTACCGGACGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCACTGCGCTTATTTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCGCTTATTTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCGCTTATTTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTGTGGGCAGTCCT GATTTAAAACTAAGACTGGCTTGTTGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTC TTCCAAATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAAACGTTTTGTGGTGGGCACCTCCTACGTCAAACATGAAGTG TGTTTCCCTCAGTGATCTGGGAAGATTTCTACGCTTGACCAACAGTTCCCTCAGCTTCCATTTCCGCC CCTCATTATCCCTCAACCCCGCCACAGGTTTATACAGCTCAGCTTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAGGATTCATGTTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTCTCTCAACATGGCTCAGAAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTGTGTTTAACTGCACCTGCCAACAAGTTCATTCATATATAAAGCATTATTTTAA CTCTTTTGAGGTGAATATAATTTATTTACAATGCTGTTAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAAAGTAAATACACAAATGAAGTGCATTATTCAA
DWU-447b	172	--- ---	---	ATTTTAGTGCTTTGCGTTAAAAAATCATGCAAAAGTATTCTGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAGTTTGAATAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTGTTAG GCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTATGGTTA
DWU-447	85	A G ---	---	ATTTTAGTGCTTTGCGTTAAAAAATCATGCAAAAGTATTCTGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAGTTTGAATAGAGCACAAGCTTAGCTAAT CAACCAATTTATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTG TTAGGCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTATGGTTA
DWU-476	63	C G ---	---	GTAAATTCAGTTTTTTCCAGTTCCTCTTTTGCTGCTCTTCAATAGCGTTTAAAGGTGAGTCGAT AAATCACTGTCATCAGGTGAGGTGCTGCTCCATCCACGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTTT

DWU-505	67 A T ---	---	---	TCATAAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAATTTCTATCACCATACAAAAATTTA[A] A/TJTGCAAGTATTTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACITTTGACTTTGAGCTTTAAACITTTAA
DWU-512	131 A G ---	---	---	AAATCCAGGCATTTGGAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAAGATGGAGAGGTGAACITGCTTTGAATATTTCCAGATGTGTTGGTC[A/G] TGCGTATGGCAGTGAGCAGGTATGTGTTTGCITTTGCTTGCACTGAAAAATTAATTTGCTATCAAGAGC AAACTATGAACGGTTTTTTTATCAAGATGCTCCAGAGTGAAGTGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAATTTATOCAGGATGTGTGGCTCATCTTTTCAGCTTGTTTCTATCTACTGTTTGT ATATACAGTTTTTTGTAAACCATATGATTGA[A/C]AAGAAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATTTCTGCTTTTCAAAATATAGTTGAACAAGATTTCCCTAAAAATTT CCACCAGGATTAAATCTCTAAAAATTTAGTCTCTGATTTGC
DWU-59	94 C T ---	---	---	CATTCTTTGTGAAAGGTAATGGACTCACAGGGGAAAGAACATGCTGAGAATGGAAAGTCTACCGG CCCTTTCTTTGTGAACGTACATTTGGC[C/T]GAGCCGTGTTCCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTTGTTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCCTAGCAGACATG CCACACGGGTAAAGCTCTGAGCTTAGTGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGTGGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAAG CAGCAGGTGCCAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCCTTCGCCTGCATTGCAGAAGGAGAGCCAGGTCCCTCCTGGAGAA[C/T]G CTGCGTTCCCGAGCCCGCCACACCGGCTTTGCACACACAGGCTGTGAGGCAGGAGGTGGGTAAAGACGT AGCTGTAGACCCCAAGCAACCAACCGCCCTGGGACCCCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTTAAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAAATCTTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTT[C/J]AAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAAGCTTCTCTAAACTGTCAAACITTTCAATTTACTGAGATTATTTTCAGGCCAAT GTGTC/TJTGTTGGGCTGAGATTGATTATCAGCTGGGTAAAGTTAACTGTTCCGTGTTCA

WI-18063	105	G A ---	---	AGGCTTTAAACTGATAACAAATTTGCCCTTTAATCACATACAAAACTCGACTTTTCATTCCTTCCTTC CCATGTTTTCTGATTTTGATGTAACTTAAATTTGTG[A]TCTTTTAAACAATATACTGTAGCTGCA
WI-18078	86	A T ---	---	AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGCTGAAGTGAAGTCAAGTTCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAG[A]TGTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C ---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAAATTCATCCTTTGTTAATTCATCAGACACTGTGGT TTTCATCTCTAGAAAGTTTGACTTT[C]GGGCCTTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18119	38	T C ---	---	GCAATCTGTAAACAGTTTTGGTAGTGGTATTACAGAGGAT[C]TTGTAAAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAAATTTGGTTCTT
WI-18142	66	T G ---	---	TTCAAGATAATTACAAATGGAAGGGGACCAATAATTCACCTTTTAAATCGAAAAATATCTATATAC[T/G]CCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCCAAAAGAGGAAAA
WI-18178	68	T C ---	---	GCATAGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCACTCCATGCCCTGGAGGTTAGTCTGGGG GT[C]CGGCGGGATGGACACACAGACACATAGATCTGGCATCTGATAGCAGGGGCATACAG
WI-18244	35	G T ---	---	TCAATCTGAAAACCTTGCTGAAGCCAGCATCTAGCACACAGTGACAGGACGTTGAGGTGGCAGAGGGCTTT GGCACTACCCGACAGCAGCATCTAGCACACAGTGACAGGAGGATGATTATGGCTGGGGAAGATG
WI-18245	115	G A ---	---	ACAGATGTCAGTTGTTGAATGGCCCATTAAGTATGGGCTTTCTTGTTAAAAGTCATCCAAA AGGCTTGGCAAGAGTTTGTATACAAACGGAGGACAGAGAAACATGA[G/A]CTGGGGAGTAGGCTCT GACAGAAAGTGGGCTGTC
WI-18261	26	G A ---	---	GATTTGAAGGGATTGCTTTATTTAAC[G/A]TGAAAAGCGTGATAGAGGAACCTGTTTAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAGATTG
WI-18268	88	C T ---	---	TAGAGGGAAAAGGAGGTGGCTGGCTGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC TTCTTACTTCCCCCATAGAT[C]TCTGACAAATGTGCTGCAAGCCCTCCAACCTGGAAC
WI-18299f	107	C A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCCAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGA[G/A]GAAATCTTTTGCCAAATTTTGACATATTCTG CAG
WI-18299e	101	A G ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCCAATTTTTT ATCTATTTG[G/A]GTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATTTTGACATATTCTG CAG
WI-18299d	77	G A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCCAATTTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATTTTGACATATTCTG CAG
WI-18299c	67	T G ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTTGCCCAATTTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATTTTGACATATTCTG CAG

WI-18299b	52	G A ---				TCACAAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAACTTG[G/A]TTTGCCAAATTTT TTTATCTATTTGGGCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAAATATTGACATATTCTG CAG
WI-18299a	48	C T ---				TCACAAAGTCAATCTCCCATCCCAATGACAGTTTGCTAAGATCATTAA[C/J]TTGGTTGCCAAATTT TTTATCTATTTGGGCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAAATATTGACATATTCTG CAG
WI-18307	76	G A ---				TCAACTGTACCAAGTTTAGCAGCAAGAGGATACTTCCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAGCATCCACGATGGTTTTATTGACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C T ---				TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGGTGGGTACTGATT TATC[C/J]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C ---				ATGAAAGTCACCTTCAATCATAAGGGTCAAGAGAAAGAATGTTTTTCAGA[T/C]TAAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACACAAGTCA
WI-18395	77	G C ---				TCCTGACATGATCTGTGAATAACGTGATTGTGGTTGAATTTCTCTGAAAAATTTGAAGAATAAATTG ATTATCAAG[G/C]JTGTCATTGGTTTATACATATCTCTCTCTCTTAATGCAAGCTATG
WI-18398	62	G T ---				TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAACAACACTCAAGGGT[G/T] GATAACATTGCCAGTATAACCATTAATCAAAACAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21	C A ---				CTCGTTGGTATTCTCTCATCC[C/A]JTTCCTTTTCGCTCTTTCTTAAATTAAGAAAAAGCAATGGAATT TTAAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTTAACTTATCAACTTGACAAAGTC AATGAAAA
WI-18409a	20	C A ---				AAGATGGGAAGAGAGAAATC[C/A]JTTCCTTACTAGAGATTTTTTTCCCTTTAATCCTTTTCAAAT TCAAAGGATCATCAAGGAGCAGGTGCAGAAGCTCTGGGGCCAGAGGCCCAAGTGCTA
WI-18442	62	C T ---				AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGAGAGAGAGAGGAAACAAAAATAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38	G A ---				TTGATGTTAATACTGTCAATCTGGAGATCGGCTAAAAATG/AJAAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAACCA
WI-18489	102	A C ---				ATATAAGCTGGAGACTGTGGAGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]JGGTTATGGCAATAGAGGTGAAAAAGAA AGGCCATATAAA
EST5b	93	A ---				CTGGTGGGAGGAAACAAATTTGGGTATATTCATACAAATGGAAAACTCTTCAGAAAAATAGAAAGAA CAAACCACTGAATCACACAACATGGACAAATCTCAAATCATATTGCTGATGGAAGAAAGAACCATTC TAAGAAATACACAGTACAT

EST5	93 A	---	---	CTGGTGGGAGGAAACAAATTTGGGTATATTATACAAATGGAACACTCTTCAGAAATAAGAAGGAA CAAACCACTGAATCACACAAACATGGACAAATCTCAAATCATTTATGCTGATGGAAGAAACCACTTCA TAAGAATACACAGTACAT
EST6	48 C	---	---	TTAGCTACTTTTCAGAAATGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTTCTTTCTTTTGCACAAAGACAAAGCAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A	---	---	GGACAGGACCTTATCCCGCTGTGCAGCAGCGGCTGATGGACTGAGGCCCGCAGGGATCTGGGCC CTTTCTCAGGGCGTCTCCAGACCCAGAGCTGTCTCTGTTTGGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCACGATGGAGATTTGGACACTGTGTGCTTTTGGTGGGT
WI-18740c	104 GT	---	---	TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTCATTACCACATGATATCCAGTAGTG[GTATAATTCATTTTGTATGGCTTCTATTTT TGGCCA
WI-18740b	96 C	G	---	TCCTCATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTCATTACCACATGATATC[G/G]AGTAGTGGATAATTCATTTTGTATGGCTTCTATTTT TGGCCA
WI-18985a	105 C	T	---	CCAAAGTCTCCTGTTCCGCTCATAAAGAAAGTTTTTGGGATGGGAGAGAATCCAGACCATCTTGGGCA GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGCACAA[C/T]GATTCCAAACACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCTCAGAAACCAATTGTGTGTTTCTCTT TGAAGCAATGACAAGCACCTTACTTTACGGTGGTTTTGTTTTCTTAT
WI-18746	114 G	A	---	GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGCTACTTGACCGTTTTATATTACTTTTGTAAATATCTT[G/A]TCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112j	212 G	A	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGTCTATCTCATGACAACCAAGAAACCGACGACAAA TCCTTTGCGAGATTTCTTCTAGTGGCTTAGAAACATGGCTTTTAAAGAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTTCAAACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A	C	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCCTCTATAGAAGGCTATTTCTAGATCATGT CTCAATGGAACACACTCTTCTTCTAGCCCTTACTTGAATCTTGCCTATATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTATTAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTTC[A/C]ATGATTAGCCGTGTAAC
WI-19057i	175 G	A	---	CCCATTTATTATAGGCCAGTGATGCTCAAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTTCTGACGGGGACTTTACCGTGACAGCGGAAGTGTATTGTACGTCCAGGCAACCGCAGCCACTG TCTTCATGCAGGAACCAAGTGCCAGATCCCCACAGCTC[G/A]TCTCTTCATCTTGGTTTGGCCACA

WI-20103	168	C T	---			TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCAAAATGATACAGATAAACTGGGATGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAAGCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGCTGGAAGCTGGGTCTCCCA/C/TTCATCTGCTCAAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTTGCACATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTTGTAAGGACAAAGAAATGGA/GA/JTTGAATAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGG
WI-19911b	116	A G	---			TGGTTACAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAAGCGT TTTAGTCTTTTAACTGAGTTTAAAAAATAACAATGCAATTTTAA/GJACACTGTTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165	A G	---			GTCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGCGAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGAA/GJAAAGGGAGTTTCCACGCGAGCCAGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGCGAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA/GJAGTTGGAAAAAGGGAGTTTCCACGCGAGCCAGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAATAA/GJATAACATTAGAAAA GCAAAATTCCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTCCACACTGGAAAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCCAGTTGGAATATGGCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTCCCTTGGAACCTGCAACCGACTGTCCATGCTGTGGGGACTTACACATTCAAGTTTGACAGI T/CJTGAAAAACCAACTGGAGCTGCTTTTCCAAAGATGTCTGTCTCCTTCAATAGGAATCCATG TTATTCTTTCTTGGCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCCCTGCCCCAAGAGCAGGAGGTGCCTG/AJAAAGCTGGGAGCGT GGGCTCAGCAGGGCTGCTCACTCCATCCCGTAAGACCTCCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGCCCTTATTGCATCCAAACACCGCCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTCTACTCAGAGTGTCTTAAAGTGAAAAATGGTCGAGAAAGAGGCACC[G/A]GGAAAGCCG TCCTGGCGCTGGCAGTCCGTGGGACGGGATGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTCTTTTGGCTTTTGCAACC

WI-20146	31 T C ---	---	---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGCT/C/C/CATTTGAGATAAAGTCAAATGCCAAACACTAG CTCTGTATTAATCCCATCATTACTGGTAAAGCCTCAITTTGAATGTGTGAATTCATACAGGC
WI-18922	74 G A ---	---	---	TAGGAATTGGTTTACGCGCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC/G/A/JCTGGCTCTAATTCACAGTGTCTTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAG GAGCCACCAGTTCTC
WI-18763b	53 A G ---	---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/A/G/TATTTAGAATG TACCATATTTTTTGTAAATTATTTATGTTTTCTAAACAAATTTATCGTATAGTTGATGAAACGTC TGTTTTTGCCAA
WI-18763a	38 A G ---	---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA/A/G/TGACGATGATGTGAATATTTAGAATG TACCATATTTTTTGTAAATTTATTTATGTTTTCTAAACAAATTTATCGTATAGTTGATGAAACGTC TGTTTTTGCCAA
WI-18771b	75 G A ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGG AACAGAA/G/A/JAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG/A/G/JAGATGTT GGGAACAGAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	---	GGGAAAAATTTGAGACGCAATACCAATACTAGGATTTTGGTCTTGGTGTGATGAAATTTCTGAG GCC/C/JTGATTTAAATCTTTTATGTTGATTTCCTTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51 C T ---	---	---	ACAAAGTCCTGTAGCCCCCTCACCTTTCTGTTTTCACATTTTGCCAAATGT/C/T/ATCGGGTTGGTTT TCTTGATTTATTTAAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	---	GTGTGTCCAAATGGGGTGTCTCTGCTACCTTGACCCCTCCCTTTCCCTCTGCTTCTCTCCTCATCA TCATTTCCCAACAACATCCTCTGCCA/C/T/JACACAACAAACGTAAAGTTTCATTTGGGCAAAAATTGA GC
WI-19970b	167 G A ---	---	---	TATAAGCCGAGTCACAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCAAC GGCCCCCGGCAGTCAGTCCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCACTGGGGGAC AGCAAAGGCCCTTCTCACTGGTTGGTCAAAG/G/A/JAGTCACCTTGGCCTGGTGCATCCACAGAGGA TGTTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA
WI-19970a	126 T C ---	---	---	TATAAGCCGAGTCACAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCAAC GGCCCCCGGCAGTCAGTCCAGCGGGGAGGAGGCTGCCGTTCTGCCAGTTCTCACTTCTAC/T/C/JGCGGG ACCAGCAAAGGCCCTTCTCACTGGTTGGTCAAAGGTAGTCACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTTGCTCACTGCCTGACATTACAGGCGAGGAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCTCTGCTCCCGAGAGACTGCCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTCTTGGGCTCTAGGCTCGGAGAATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAAA[T/GIACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGCTCACTGCCTGACATTACAGGCGAGGAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCTCTGCTCCCGAGAGACTGCCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTCTTGGGCTCTAGGCTCG[G/C]JAGAATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGCTCACTGCCTGACATTACAGGCGAGGAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCTCTGCTCCCGAGAGACTGCCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTCTGGGCTCTAGGCTCG[G/C]GGAGAATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGCTCACTGCCTGACATTACAGGCGAGGAGGCTGCTGCAGCCTCC[G/C]GCTGGCTGTGCACATTCCTCTGCTCCCGAGAGACTGCCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTCTCTGGGCTCTAGGCTCGGAGAATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAAATACATAGTATTCTTCTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19106	247 T C ---	---	TTATCCAGCCCTACCTTGTTAGTTATTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCCTCCACGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCCTCCTATTTTAA[T/C]TGG
WI-18944	147 A G ---	---	CAAGGCAAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATATGTAGCTGAAACAAA AATGCCAGAAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTTACCTAGCATTTCAAACCC AAATGGCTAGAAC[A/G]TGTTTAAATTAATTTACAAATATAAAGTTCTACAGTTAATATGTGCATA TTAACAATAGCCCTGGTTCAATTTCTTCTTCTTAAATAAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTAAAGTGAAGGATTGGATGATTGTTTCATAATACATAAA GTTCTCTGTAATTACAACATAATTATTATGCCCTCTTCTCACAGTCAAAGGAACTGGGTGGTTGGT TTTTGTGCTTTTGTAGATTATTGTCCCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTTA AAATAATAAACTTTGGGAAAAGGTGTAA[G/A]ACAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCAGGAAACTGGAATAAGCCTTCGAAAAGAAATTTGCTCTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAAGTGTGCTGATTTTGACCTTGTATTCAAGTTAACTGTTCCC CTTGGTATTTGTTTAAATACCTGTACATATCTTTGAGTTCA[C/T]CTTTAGTACGTGTGGCTTGGTCA CTTCTGGCTGAGGTGAAGACGTGCTTGGAAGACAGTCTGGGCTTG

WI-19042	193 A C ---			TTTGTGAGTGTGCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAAGTCCCAACAG ACACAATTTATACTGCGACAGAACTTCAGCATTTGTAATATGTAATAACTCTAACCA[AC]GGCTG TGTTAGATTGATTAACATCTCTTTGGACTTCTGAAGAGACCACCAAT
WI-18984	208 A C ---			ATTGGCCCTGTACAGTTTGTCTATTATAAATCATTAAAAACACTACAGGTGTGAATGGTTAAAA TGTAGGCTCCAGTTTCTAGTTATTTCTGAGTGTGACAGAGTATTCGCACGTGATTAAT GTAACCTTATTAAATGAAATCAGAAGCAGTAGACAGATTTGGTGCAATACAAATATTGTGATGCAAT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---			GCTTCAATTGGCGATTGATTCAGTGCCCAATGTAAACAGGGTGGTAGTTGTTACTCAATTTTGAAT ATACCTTTTCTTATTGATTCT[A/G]TAATATAGGATCCTGGAATGAGACCTGGTGGAA
WI-18821b	76 T C ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGGCCCCGGGGAACCTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---			TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCCGGGGAACCTTGCCAACTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---			ACTCCTGTGCTGTGCTCACT[G/A]CTGTCTTTTGAACACAGGAAAGTCACAGAGTTTAAAGAGAA GCAATTAACATCTGAATCGGGAACAAAGGTTTATCTAATAAGTGTCTCTTCCATCACGTTG CTACCTTACCACACTTCCCTGTGATTTGCGTGAGGACGTGGCATCTTACTTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTG
WI-18908	70 G C ---			TGGAAATTCCTTTCATCTGGAACCATCAGAAACACCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[G/C]TTAGGGAACACATCCATCCTTGAGTCAAAAAATCTCAATTCCTTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---			CACGGTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACGCCCTGTATGACCCGCAATA TCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCATTTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---			CACGGTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACG[C/A]CCTGTATGACCCGCGCAA ATATCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCATTTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[A/A]AACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---			TTGAGGAGGTGGGTGAACCTGCTCTTGGCAGGGATTTGTGACACTGCATTGCTGGGCTGTGTCCTT/ CJCGGCTCTTCTGACCTTGACCCGTGGATACCAGGCCATGTGCCATGGTATTTGGGTCTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	---	AGGCTGTGGCTTATGTCACCAACAGAGGGTCTGTAGAAGTCTGGCTGCCTGGGATGCCCTGCGC CCCTCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGAGGAGAGAGTGTCTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTGAACACCTGAGGCCCTCTGTGGCCACCAGGCACTACGGCTTCTCTCTCC AGATGTGCTTTGCCGTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	---	GTTTGAAAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTTCATCTCAA[C/A]CTCAACACTATTGAC TTTTGGGCTGGATAGTTCTGTGTGGGGTTTGTCTTGTCACACTGTAG
WI-19016a	161 C T ---	---	---	GTTTGAAAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGAG[C/A]TGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTGTGTGGGGTTTGTCTTGTCACACTGTAG
WI-20096	21 T C ---	---	---	GGTTTGGGGCATTATTTC[C/A]GATAGAGACTGGCACAAAGCTTTTGGGCTAAGGACACCCGCCCTCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAAGCCCATG AGTAAAGATTAAAGCAGTTACTTTTGAACAAAGGAGTGGCATAAGCAACTCAGTGTGCCCC CTTAGGGTGGGAGCTCTCC[C/A]CTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAAT/AJATAAGGTAACCTCAAAGC CATGAGTATAAGATTAAAGCAGTTACTTTTGAACAAAGGAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTCCCCCTACCACTCCCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	---	TCCTCAGCTCTGTCATCCTTGTCTTGAGGGTTCTGTGTTACGGCCCCCTCCAGGCGATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAGCCCCAGCTCTCTAGAGGCTCCA[G/A]TCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTTCGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTCTCCCAATGTCCTCCCCGGGGG
WI-20860	224 G A ---	---	---	CTCTCCCCTAAGGAGCCTTGGCCTTGACGCCCATTCAGCAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCCTGTCTCTCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGACC GGAAAGGAGGGCGGTCATT[G/A]GGTGTAGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	---	GACGTGGACAAAGGAGGTTTAAATGAATACCTTTTGTTC[C/A]TGTTCAAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACCTAGGTTAATAATAA GGCTATTGTCCACCCACTCTCGGGCATGCTGCAATATCTCGGGCTCAAGTGGGAGGCCACGTG GGAACAAGGCCCTCAGAAAAACAAGGACATGCAGCCTCCCTGAGCCAGTCTCT

WI-19766b	93 A G ---			TGGCCTCAATGACTGTACATTGGAGAAGCTGTGCAGCAGCATCTTTCTGTGGTGGGAGGGCAGGAGATGAACCATAGGAGCCAAAGTC[AG]GACAAACAGAGAAGGACACCAAGCCTGAAACCCCTCGGACACAGAGATTACAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCTCTTACCCTCCTCTACACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---			TGGCCTCAATGACTGGTACATTGGAGAAGCT[GA]TGCAGCAGCATCCTTTTCTGTGGTGGGAGGGCAGGATGAACCATAGGAGCCAAAGTCAGACAAACAGAGAAGGACACCAAGCCTGAAACCCCTCGGACACAGCAGAGTTACAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCTCTTACCCTCCTCTACACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---			CTTCCTCTGTTGGCTTTGCAATTTGTCGATTGGAAAAACCACTTGAAGAAGGACTTTCTCTGCAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA[C]G/AAAGCTTAGAAAGGAACAGAAATTCCTTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCAGGCCTTATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---			CTTCCTCTGTTGGCTTTGCAATTTGTCGATTGGAAAAACCACTTGGAAAGGAGGACTT[GT]TCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGCTTAGAAAGGAACAGAAATTCCTTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCAGGCCTTATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---			GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCCATAACCCCTTCTACATTGGAAAGAGCACACCTTGTATACAGAATGGCTCCGTGAAGTCTTTTAAACGGACAAAGGTAAATCACAGCTAACAAACGTTGATGTTGGCTCACACGTAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAGTAAAGGGCA[C]G/TTCCAAAGAGTAACACTGCTA
WI-20679	82 T C ---			TGTTTGAATAAAAATTCATGGTCTTAATTGAACCTGTATGTACTTCTTTTGAATATCCTTTTTCATTAAAAATAAT[TC]TCTAAACCACTCTAIGTGTTCAACCTTCTGTTTAACTAAGATATGGGTTTTGGAAAGGCCACAGTCACCACTCCATGAAGTGGGCGAATGGTCTTGTTTTGGAAAGCTCTCAGGGTGTCTCTCCAGAAA
WI-19909a	29 T C ---			CCAGAAATAAAGCCTGAATATCTCTTTCT[TC]TAAATAATAATTTTCTCTTTGCTCTTCCAAAGTAAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGGTTTTTCTCTTATACCTTGTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---			TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTCTTAGGGGCATGAGACATTAGGAAGGCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTAGCAGGAGGAGGAAAGTATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATATTTGGGTGACGTCATGCATCCCCCATGCATTGGTTT[GC]ATGTCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60	T C ---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTAGTGAATGAGCAAAAGACCTGAAATACTGTCJGGA AACAGTAAAAGCAAATACCACACAAATTAGGAGGAATATTATTTTCAGACATAGGATATTTAAACAT CACTCAAAATACCTGGAGCATGATTAGCAATAAATCTATCCATAAAACCAAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATCCGTATT
WI-20895	107	G C ---	---	TGATGGCAAAGTACAAAGGCTCTGAAAGACAGAGTAACAAGAGCAGCGCAGCGGTGTGGC CACTCCCAAGCAGGAGAACACTTGACTTCAATTAAGGCAAAGCTCTTACTCTGTTACTTTTCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGCTCCTAGGAA TATAACTGGTACTATAGGCAAAACAGATGCA
WI-20721	72	T C ---	---	CCGTGCAATCACAAAAGTGGAAGTGTGATATTTTGAATCATACTTGATTAAACCACCTTCAGAAA TTCTATTCJAAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161	A G ---	---	CTGGATTTTAATATTTCTGGCCTAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTCTGCTAACATGTTTTCGAAGATCCCTAAGTAAGGTATTGACGACTGAGACTAGTCGGGCAAA GTCAATGAGACCCCTTAGCTGATCTCATAGJAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCTCG
WI-19348c	103	C T ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAAGGATGGGCAATGCACCTCTG GCGGTCGATGAAGAGACTGTTGGTCATGGCGGTGAJCTGCTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTTGTAGAAGCTTCTCC
WI-19348b	98	G A ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAAGGATGGGCAATGCACCTCTG GCGGTCGATGAAGAGACTGTTGGTCATGGCGJAGTGACGCTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGTTGTAGAAGCTTCTCC
WI-19635	98	A T ---	---	ATTAGTTCGTGTTGGGCCACATTCAAAGCCATCCACACAAGCTCTTGTAGGCCATTGTAAACAATG TTAAAAGGTACAGTAAAAATACAGTATTATJATCTTATTGTGTAGCACGGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTCTGAAAGAACTTTTGCCCTT T
WI-19641a	46	A G ---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJAGJTATTATAGTCTCATGTTT TTAATTTATGAATAAGCTGCTGATTCATTGATTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAATAAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A ---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCTTCJAJGGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGATGGACACAAGTTTTCATGCTATTA
WI-19673b	180	C T ---	---	TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACTTCTGTGTCATTGCGCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACCTGTAATCTAATAGT GAAAAGGCCAAATGATGCTCAGTATCACTGTGAAAAACATTTTTCJCTGTGGACCAGCTGAAAGAA TCTTGAGGAGCCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC

WI-19673a	35 G A ---			TCTGCCATGATCACAATTGTGATGAAGAACATGATG(A/J)TCACTAGTAGGTAACCTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTTAOCCTACCCCTGCTTTTGATCACCACCTGTAAATCTAAT AGTGAAAGGCAAAATGATGTCAGTATCACTGTGAAACAATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAAACACAGCCC
WI-19724	35 A G ---			TTTATTTGGAAACAAAGGATTGTAATTTGGGTAA(A/G)CTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACAGAGATTTTGGTTTCTCTT
WI-19307	196 T C ---			TCCTCTCCCCCAACTAGATGGTATTGATCACTCTGCCCAAAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTTGCCCTTCATGAGAAATGGTGGCTGGATGGAGGTGACATTCCTTGGCTGT GGTGAACCTGCAAGAAAGGAAACCCAGGCAATGTATCCATAGAGGCCCTTAAAGAGACCCG(T/G)TGG AAATGGGCCATGGTCTAAATTTGGTGTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85 A T ---			CTTCCCTCATCCCTCTTCCACCACACCATCCCGGAACAAGTGTCTCCAGGATTCCTGCCACTGGC CATTTTGGAGTGTCC(A/J)TTGGTAGCAATGTGGAACCCACAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGAGTCCAGAGGGGCTTATTGAGGGCTTTGCCACTTGTCTCATAGGCGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCAATCTTCCCGGCGTAGGCA
WI-19946	122 C T ---			CAATGGACTGAATGAGTGCCTGGTGGTGGGGCACACACACCTTCAATACACGTCGAAGGTGG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGCTGAGCGACAGAGAGGT(C/J)TCTTCCCTG ACCCAGACGCACTCAGAGCCAGGTCCTGGTTTCAAACTGCATTTAACCTGCCAGAGAGGTTTAC CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 G A ---			CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAATATACATAAGTAACCTTACAGCACACATTTTTAGGGCCCAAGTTTGGATCTGTCTGGACCT CAATGT(G/A)CTCTCGGAGAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCTCAA GTGATGGCCAACAGAGCTTCTGAACTCCTCCTGGGGAGGTAGCTGACAAG
WI-19076	40 G A ---			TTGGTTGGATACCTGCTGGAACCAACCAAGCAGTTTAA(T/G/A)GTATTCAAAATACCTTTTAAAA GTATCTAGCACAGAATTTTCTGTAACTAGATTATGTTGTAACTTTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCCTATTCCAAATCTATCTTGGCTCCTGAAAAACTGCAGA AAGGCATTTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATCTT
WI-20218	26 T C ---			CCACACACTCTGGTTTTATAAGCTA(T/C)JAGGACAGAGCAGAGATGGAACTGAAAAACAGGGTAG AAAAAACAATAAATTGGAGGGGAACAGTGGGATGCAGAAAGAATGACAACAGCCACATGTGCCCA GTCAAAATACCTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 T G ---			CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCCAGGCTTGAATGGGGAGGGCTGGGCTCTACCCCTTCTCTTCCCA TCCAGTCTATTGCCAGAT(G/J)CCAGAGAAAGCGGGAGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTCACTTCTGTGCGACTCCTCATGCTGGGACTTGCTTTCGGG

WI-20361a	192 G A ---	---	CTGGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGGCTTATGCAAGATGACAGAATATGTGAAATCTGATTGTCCAGAGATTACACTCTGCACTCCCAAAGCTACAACAGTGCCACAGCTGAGAGGTTTCCCTATACCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC
WI-20572	75 A G ---	---	AAATGGGAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCGG GAGCCAAACCCAAACAAATAAAACAGAACTCTTTTGTAAACTAAGTCATACCTACTCTTCTCTTCATGAAT[G/G]TCATAAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTTGTTCAAAATTAATTCATCTTTCTCAAATTTTAAATTTGTTTAAATCCCAAAGGTGCCATTGGAATTTCTTCAAAAATAA
WI-20588	133 G A ---	---	AACAGCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATCTTCACTTTTTAAGAAAATGTGAGATCCTTTGTGGTTTTTATTTCCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCATTCAAG
WI-20593	79 A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTGCTGTACTTCAG[G/G]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAAGCTGTTAAAGGAACTCAGGATGTTGTAGGAAGGGGAGTGGATGCCAGGCTTCAACAGACTATCCAGAAGCCATTCCATGGGTATTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57 T C ---	---	TTCTTTGCCAAGCCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCCTCA[T/C]ATGATCTGTGCCCTGCTGCTTTTAGTTAGCAAGGTGTATGAATACTTTTAAAGTTTGTGTTCTTTTCCCTCGTGGTATCAGTGAATACTGATCTATTCTCTGGTAGGGTCAATTTACAAAATGGCCATGGAACTGAGC
WI-19066i	239 A G ---	---	AAAAGGCCACGTGGGATAAAATCACTACCAATCGACGCCACAGTATT TGACAAGGGAGAGAGGGAAATTTACTCATTTGCAAGGAAATCCTCACITTAAGCTTCAGTGAGCCAC
WI-19066g	184 C T ---	---	AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCCATATTC[G/TTGGATGCTCAATTACAGTACCAATTGCAGGCAAACTTTTTCTTAAACGCCCTTCACTAGTTTCTTTTTA
WI-19066f	148 T C ---	---	TGACAAGGGAGAGAGGGAAATTTACTCATTTGCAAGGAAATCCTCACITTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATAATGTTCTTGCGT[C/TTGGTCAACCTGTAGCTGAATTAATCTTCCATATTCGGATGCTCAATTACAGTACCAATTGCAGGCAAACTTTTTCTTAAACGCCCTTCACTAGTTTCTTTTTA

WI-19066e	147 G C ---	---	TGACAAGGGAGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAAGTGG CATATGTTCTTGCG/CJTGGTCACCCGTAGCTGAATTAATCTCTCCATAATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAAGCCCTTCACTAGTTCTTTTA
WI-19066c	100 G A ---	---	TGACAAGGGAGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTAGCTGAATTAATCTCTCCATAATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAAGCCCTTCACTAGTTCTTTTA
WI-19066b	87 C T ---	---	TGACAAGGGAGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTAGCTGAATTAATCTCTCCATAATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAAGCCCTTCACTAGTTCTTTTA
WI-19066a	72 C T ---	---	TGACAAGGGAGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTAGCTGAATTAATCTCTCCATAATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAAGCCCTTCACTAGTTCTTTTA
WI-20660	105 G C ---	---	TTTACAGCGAGTTTTCCGCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGATATTTGTC/GJTAAATAAGGGAAGCAATTAATATTA CAGACATAATTTACAAGGTTCTGAACATGAGTGATCCACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCCGCCCCCAAAATACTGTTTAAACAACACTATGTTTTAAGA CTGCTGOCAGCTTCTCTTTGGCCCTGCTCCAGATGGGGTCTCTGCGAGCCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCCTGCTGCATGTCATGTCACCCCTTGGTTC/JTTCGCTCCATCGGC TTGAAAGCTCTGAA
WI-18768	120 C T ---	---	TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGT/JGJTATTTAACTTCTAGTTGCTCTTGTCTTG GTCCTTCTTCCAATGATGCTTACTACAGAAAGCAAATCAGACACAAATAGAGAAGCCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAAGTCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-19087	37 A G ---	---	GAAAGCCAGAGATTAGCCCCGATTCGGCATCTGTCAACCCAGGACAGAA/JGTCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTGGAGATCAGAAAAATTCATATTAAGCAAAAGTGATACAAACA CAGTGATTGGGAATGCCT
WI-18790	49 A T ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC/GA/GTGGCCAAAGCCAGACACTACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTGAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTGCACAGCCCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA
WI-18987	35 G A ---	---	

WI-18919	26 C T	---	---	TGGATGAAACCACAGGGATTCCGGA/C/TGCCAGACCCCATTTTATCTCACTTTTCTCTACAGTG TTGTTTGTGTTGTGGTTTTATTTTATCTTTTGCCATACCAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A	---	---	CTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCCTGGATGAGGCTACTGA
WI-18741b	38 G C	---	---	CTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAATTTTACAAGCCCTGGATGAGGCTACTGA
WI-18741a	23 T G	---	---	CTTCTGGTCAAGGCTTGGACAT/GTCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAATTTTACAAGCCCTGGATGAGGCTACTGA
WI-19179a	170 G A	---	---	TCAGAAGCAGACATGGCATCTGTTCCCTGCTTGGTGTGTACCTTTACGAGACCTGAATT TTAGAAATGCCAGTGTGCCAGAGTGAGTGAGTAAATCTCCTTTCAAGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTATAAACATATCAACCA/GA/TAAGCATTAAACCATTTTATTTCTGTGCTT AGTGCTGAAGATGCTCACCAGTTTTCTGTGACAGTAAGGACGATGCT
WI-19212	46 T A	---	---	CCAAGTTGCATCCATGTTTGATTTCTGATGAGACTAGAGTGACAG/T/A/GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGAGATGGCCTATGGAATAATGACAGCTGC ATAATTAACACATTATCAAAGTCCCTCTTACAAATTTATTTCCGCGAGCATGTCAAGTAAGTAGACCCA ATGGGGAGAGAAAATGCCTGCTTTCTTCCCTCTTTCTGCACTGCCATAI
WI-19183	210 G C	---	---	CTGTTGAAGGCTTCTCAGGCAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGTTTCTCCATTTTATGGGATGAATAATGTGGTTTAGAATAAGGAACAAGCATTAI CCTTTGCCAACAGCCTCACTCTAAGAGGCTTTTGTCTGAGTCAAGCAACACTTGCTGCTGTGCC CTTGGAG/G/CTGCATTTGACCTGCTCACTGGTAAGTGACTTGGTGGC
WI-20014b	214 T C	---	---	TTGAAATCCCAGTCTCTGCCCCCAGGCGGGTCTGTCAACATAGAATGTCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAAACTTGGCTGAGATGTTCTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGCAATGTTTCTTGTAATCTGAAACTGGAAACTGAACCAAGTTTGGCTTTCTCTAGTCACC AAGCATACT/T/CTCCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C	---	---	GTCTCCCAGAGTGTCTTGACCCCCAGCCCCCTGTCTGCTGTGAAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGCCTTAGTTTGGACATGCTGGGTAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCCAAGCTCATCACACCAGGGGGCCATCCTTCTCAATACAGCC/T/C/G CCCTTGCACTCCCTATTTTCAAAAATAAAATTAGTGTGTCTTGCCTGTCTGT
WI-19135	20 G A	---	---	CAGTTACCCCTGCTTTGCCTC[G/A]AAAGTGTCAATTTTGTAAATTTAGTATTAACCTGTAAAGT GTCTGTAGGTACGTTTTATATATAAGGACAGACCAAAATCAACCTATCAAAGCTTCAAAACT TTGGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACT GCTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	TACACAGAGGTCGCACCTGGACTCTGAGGTTGGGTGTGGAAGGGGAAAGG[A/G]ATGGAGAC CTGCTCCCAAGCTCTTCTGTAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGAGGT CACCTTACCCCTTTTATAGGGAAGAGTGTACACTCCTGGCTATCTCAGGGGAATGGGGAAAG AATCTTCAAGGGCAAGAACTCGTGGGAGGATGTCGTGTATGTATACT
WI-19144	222	G C ---	---	GTGCCAGTCTCCAGAAAGCAAGACTGCCCTTCATTACGCCCTGCTGACCTCCCAGCCCTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGTCCAGCTTGTGAGCTATCTATATATTCATTTCATAGCCAA ACAGGAGACCCCTTTCAGGACTTGCACACAGGAGGCTGTAGCCAGGAAACCCCTCTCTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTCTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACTAG[C/A]ATTTACCGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA CTTGGCAGATGCCTGACAGAGAGTGGTTGGCAGACAACACTAGCATTTTCACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGTCTGTGTGAAGCCACCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGCTTGT[C/G]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCGTGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTCACTGCCCAAGTATGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTGCCTAATGTTTCACAATGGTGAAG[A/G]GCTTCATGTAATATGATCAGGACCCACC TCCAGTCTTCTGAAAGTGTGACAGTGTCCAGCGGTTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTACCCAGTTTAGTTTGGGATGATTTGATTTCTGTTGTGATCCCATTTCTAA CTTGGAAATGTGAGCCTCTATGTTTCTGTAGGTAGTGTGTGGGTTTTCCTCCCAAGGAGT GGCAGCATCCCTCTCTCCCTAAAGGGACTCTGCGGAAC[C/T]TTTCACACCTCTTCTCAGGGAC GGGGCAGGTGTGTGTGTACACTGACGTGTCCAGAGCAGCACTTT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACCTAAGACAAGAACATTTCTCTCATAAGACATTG ATCTGTTTACAGGAAACAAACCTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTCCTAAGACATTTTTCATTCATGAATATTTCAAGTTTTCATACTGTACA CATTTCTAAACACATGATACCCAGCAGCAACTGAAATGAATGCCGAATTG

WI-19134c	263 C T ---		CTCCTGTTCTGACCTGACAGGGTGACACAGCCCCCTTTTCACACTCTGTCCCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGCAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACCTATCTCTTTTCAGAGCAC TTCATCCACTTGTCTCCTCCCTACCCCTCGGCACCCCTGGGTGGGAAGGG
WI-19134a	162 T C ---		CTCCTGTTCTGACCTGACAGGGTGACACAGCCCCCTTTTCACACTCTGTCCCTCTATCTTCTCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAAGAGGGGTGCAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATTCAGACGGTGGCTAGAGCCAGCTGCACCTATCTCTTTTCAGAG CACTTCATCCACTTGTCTCCTCCCTACCCCTCGGCACCCCTGGGTGGGA
WI-19224	112 C T ---		GGTTTCACCAGTCTTCCAGGGAACCTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCTCTCAGGATGCCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAAGTTGTCAATCCAGCAGGCCAGAACACTTCC AGGGAACTCATTCAGGAGGTGAATAATGATGGATGACTCTCCCAAGATGAATA
WI-19201	179 T C ---		GCAGCTCTAAGGACCACCTGGCCATTAGCTCTTGCTTTTGATGGCATCTCTTCCACCTTGTCTTCTC CTTTGCTCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGCCCCCACTTTGCCTGCAGGTGCACCCGAAAGGACTTCCTGGGGGATAAAATTCAAAAA GTGTGATGTGCTGCTCAGAAGGTGAGACTCCATGCTGCCTTGGCCTCAA
WI-19034	45 T C ---		GAAATGGCTCCACTCAGAGCTACCCGGTGTAGGAGTGGGGAATTCJACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAAAGGTTTTACAGTGTCTGCTGTTGAAAGTGCAATATAAAATTTTGTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTTCTGTCGAATTGAC ATTGCTACTTATAAACTTAGTCCCTAAGTCTTCTTATGCTGTGCTATATA
WI-19102	25 C G ---		TGTTCTGAGTCACGCTGAGGAGAGTCGCTTCACTCAGGAGTTCATGCTGAGATGATCATGAGTTCA TGCGACGTATATTTCCCTTTGAAACAGAAATGAAGCAGAGGAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTAGTTTGAAGTCTAGAACTCCTGTAAGTTTTGAACCTCAAGGGAGAAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCACTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---		AAAGGAGGGAGAATCTTTTTACATAAAATGCCCTTGATCATCTCCAGTCCCTCACTGGGGGAJA/A GJAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---		AAAGGAGGGAGAATCTTTTTACATAAAATGCCCTTGATCATCTCCAGTCCCTCACTGGGG[G/AJA AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---		GGCAGCAGCTTTTTAATTTGAACACTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTCJAAAGATCCACAATTCGAAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121 C T ---		CAGAGGGAAAAAGTTTATTGATCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGCCAGGACAGAGGGGGCGCTGGACAGCA GCGCATGCCACAACATTCA

-257-

WI-18017	87	C A	---				ACAAAGAAATGGAAATAGGTTTGGGAAACCTTATCTGCAATGTACAAAGTAATCCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTTCAATTAATAATATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G	---				TTATTGGCTTCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTTCAGAAACCTTCGATTCTGAATATCCC[A/G]TGGCGCATATGCAAAAGGAAGATGA
WI-18254	64	T C	---				TATACGGATCATGTATTGTGTGACCACCCTACACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]]GCCAAATTCCTCTTCTTCTTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTCTAGACATTT
WI-18265b	117	C A	---				CAATGGGTGGACTGAGTATAAAACGCATATTGAGAACAAAGACGGCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG[C/A]GTTTTCAACCTTTC CTTGGGIGGTTTCTTCAG
WI-18295	40	C T	---				ACCACACATTTGTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATCCCTTNCCTTAGCTTCATTCATATATGCCCCAA
WI-18459b	64	T C	---				GGGCAAGAGACAGAGATTTAATTGAATAAAACCTCCAGGCTGTGACACGGGTGGGAGACACAA[T/] C]GAGTAATTAAACAACATAATATTTANATGACAGTGCAATTAATTAACGTCTGGGTAAAGCCAGAG GGGAGGAGGGGCTTTTCA
WI-22585	56	A G	---				TTATTTTAAATTTGCATCTGAGATAATAAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAAGC AGCAGTGAAGTTTCGGAGAGGCAGGTATCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A G	---				GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC[A/G]TCTGTGAGAATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---				GCCTTTGCTCTTTGCTGCTCTCAGAGGCCTCAGATGGATAGCAGCAACTTCTTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAGA[G/A]GGATCCAGCAGTGAGATCAGGCAAGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98	C T	---				GGCAGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTTTATTTTATGATGATG AAATATTTTGGAACTAGAAAGTAGCAGTG[A/C]TJTGACAACGTTGTAAAGATATTAATGCCCCT GAACTGTTTCATTTAAATGGTAAATTCATGTTATGTGTATTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAAGTGAACACAAG
WI-21485	82	C T	---				TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTTCAGCACCTAAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TJTGTCACACAGTACAGTGACACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---				TCAGAATTGCTTTCCTGCTCCCAACCAACCAAGAAATTAATGAATGCNCTTACAATTGAGATGACTT GAAAGTTAAAGAAAGGTACCTTCCCTTGGAGGTGATGACAGGATAGTCTCTCTGTTT[C]CTTGGT GCAAGTTTGAACCAGTGATTATGTACCATTTGCATCAGAGCATCTGTTTCCCTGTGAGATCCCCACTAG

WI-20561b	94 T C ---	---	CGTTGCTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATG TACTTCAGATGAAAAATCCTTACATGTC/G/GGAATCAATGTCCTTTTAAATTTTCAGATAAAGAATTT NCAITTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---	---	CGTTGCTATTAAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCCTTTTAAATTTTCAGATAAAGAATTT NCAITTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---	---	GCTTTCATTTCTGTCACCCACCTGTCACCCAGTTATGTTGGCCTTCAATATATGGCGT[A/T]AGAA A[T/A]ATAAATCTATATCATATATTTATACACACAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20116c	59 T A ---	---	GCTTTCATTTCTGTCACCCACCTGTCACCCAGTTATGTTGGCCTTCAATATATGGCGT[A/T]AGAA CATATATAAATCTATATCATATATTTATACACACAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20116a	22 C G ---	---	GCTTTCATTTCTGTCACCCACCTGTCACCCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACACAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI-20466b	133 G A ---	---	AAAGATTTGCAGTCCCTGGGACACAGTTTGGAAAAACACTATTTATAAGGTTGCACATATTACAAACAG NTCCCAAATGGTGAAACTGGTATTTCTAAGATGAAAGCTTAAAGACATAATGAAGTGAATAAACGC G/AJTGTAACATAATGTTTAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39 A G ---	---	CTGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAACIAGIAGTTCTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACTTATTGGAACATACTTTGTAATTTATTCGAGGAAGAAGAAATCT ATAAGATTGACTTACTCATTTGTTGACTGGTTTTTTGAGGCTTACTGGGG
WI-21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGAT/C/GCCTAACCTATCTCAATTTTAAAGTAATGTAGCAA
WI-22091c	205 G A ---	---	GGCGTGATTTGATGCAATGTCCAAACCAAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGCAATGTAAACATACAAAGCATATTACCTCCCCCTTAAAGTGAATCATATTTT ATTACTTGTGCTGTAGCTTTTAAAGGTTTAAAGTGTAGCATTAAGTGTATTACTTGAGGGCA ACA[G/A]AATTACGGCTTAAACAACACACTAAATCATGAGGCTCAGGGATTG

-259-

WI-21805a	45 A T ---			CAACTGCTCTGAGGCTCTTCACTAGCTGATTATAATCCTATATTAT/AAAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTTCTCAAGGGTGGATATGTTGGGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGTCTTTTGTAGCTTAAGTCTGTTTGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTTTGTAAATGCTG
WI-21778b	155 T C ---			AAAAATCCATAATATTGAACCCCAAGTTACAGAGAAAGTTCTGTAACITTTTTTATTGAATTAATTGAC TCTGCCCGCTGTCTGCTGCTTCAACTCCAGTCTGTAATGCCCTGTGTAGGTGGGTCCCCAG GTCTGGGCTTCTGAGGTCTTCTGAGTGAAGAGGGCAGGTGGT
WI-20907	241 A C ---			TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCCGGAAACACTGTGCCTCT CAATGATCTAGAGCTCATCCTTGGCGTACATGAGGGCAGTTGTTCTTAGTACCCATTTAGCCG ATGGCTCTCAAGCCAATTCACACTGGGAAACACACCCCTCACAAGATGCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTTA/C/AAATTATCTA
WI-21449b	222 C T ---			AACAGCAGCAGTCACCTCCAAATGCAAAAAAATTACAAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACAAAGATCAATCAGCAGCACTGGAGGGCTGGAG AAGCCAAAGCCACTGGTCAGGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/C/TJTGACAGAGCCAGTGTCTCTGGGTAG
WI-21558a	157 G A ---			GCTTACAAGGAAGCCTGTGGACAGGCGAGNTGGTGGAAACGACTCCAGCTGGAAAAACCTGCCCTC CCATCCCCCTTAGCGCTTCTTGGCTTCCGGCTGATTTCTTCGACAGCAGTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGACTCCCTCCACACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCCGTGAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGCTGGCTAGCAGGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAACCAAAACAAACAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/AJAAATTTTCATGAAAAATTTCC CCTAAACCATACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGCTGGCTAGCAGGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAACCAAA/C/A/CAAAACAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGGAAATTTTCATGAAAAATTTCC CCTAAACCATACAAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21609b	146 G A ---			TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAAACGTGCAGTCCGTTTCAAGCTGTAAA AACAAAGCCCAACCCAAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAG/G/AJAGGGTCCCGGTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI-21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAACAAAC/TTGTGCAGTCCGTTCAAGCTGT AAAAAAGCCCAAAACCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAAAGGAGCCTGT AAGGATGTTTCAAAGGAGGTTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGAGTTGGAG
WI-22512a	104 T G ---	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTCCCTCCCTAGGGCTTCA GGTAAGCCCTGACATCATGGTCTTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGTCTAAGGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139 A G ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCAACAATTTCTGTCCCTTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTGACAGGG TTTC/GJTGCACTGGTACAGAACAACAACAGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAAT CTACGG
WI-21028a	121 A C ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCAACAATTTCTGTCCCTTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTGACAG GGGTTTCATGCACTGGTACAGAACAACAACAGGGAGTTTCACAAATTTTTTATACAAATGCTTGGGAATC TACGG
WI-18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGACTTCTTG/GJTTTCA TCATACAAGACAAGCACAAAAAGCACCCACCTCTGAGGAACATTGGACCATTGCACCCCTTGAAA AA
WI-18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGTT/AJAATAACTTATGTGACTTCTTGATTTC TCATACAAGACAAGCACAAAAAGCACCCACCTCTGAGGAACATTGGACCATTGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAGCAAGGA GCACAGGTAGTCCACAGAATA/GA/GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAATACTAAGATTAGATGAACAACAACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGAGGAAC AGATGTTAACAAAAACAATAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59 T A ---	---	CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCA/T/AJACAT TGGCTGGAATGAGGTGGTCAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI-22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTTCCCTCTCTCTGACAC CAGCAAGGGGAGGCACCATCACCGGCCCTGCCCATCATGCATCCAATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGTCT/GJTGTTTTAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC

-261-

WI-21661	117	G C ---	---	---	GCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAAATAG[C]JTTTAGTCACAGTC ACACAAAACACTACCTTCTAAGGAAAACGTCCAGTGAAGCCGTAAATTTTGTCCTTCAGCTATGAAG GA
WI-21980a	25	T C ---	---	---	TCAGTTTAAACACACATTCATCAAGGA[T/C]JAGATTAAATTAATGTCAAGGTGAGCATAAAAGGGAGATT TAAACCAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTTTATTAAATTCAT GGTGAAGCCCTGGGATAAAG
WI-21636	71	A G ---	---	---	TGCTTGATTAATGTGGTGTACATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTTT AAA[A/G]TAGCAATATCTATTATATAAATAATTGAAATAACACCATAATAATATCACAAGGA AGTAATCTAATTGTGTTGATTTGCAGAGGGGAGAAAACATTACCCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112	G A ---	---	---	TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACATCATTAGA CAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACATAAG GAACAGAGTCCCTGCTGCTGCTGCTACCC[C/T]GATGATGCTTCTCTGCAATGGACTATTTGCC AAACCCACTGAACCTACCCAGCTGAAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97	C T ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGACGACCTTCGCGTCATCTAT AATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35	A C ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCCTGATGACGACCTTCGCGTCATACT TATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32	G T ---	---	---	TTACCTTCCAAACAGGCCACTTTGGAGAAAG[G/T]AAGAGAAATGCTATTAAATCAATAAGCCAAGAC AATAGGACTACCTGGGTAGACCAAGATGGGAGTCAACCATACCATCATCTCTGCCACAGAACC TTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTT CTTTAGGG
WI-21703d	197	A G ---	---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGATAGGAGGTGGTGGTGGCAGGGCTC TGATCCCCCTTCTCAGCAGCAGCACCCTCTCACCCCTCTGGGAAAGCAGCATTTGGAGCCTACACCA CTTGCTTTCTCACCAGGGTAAGAAATGCAGGTTATTCAGAGGGGAGTGAGTCTGGGAA[A/G]G TGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGAACTTGTGGGGGAAGAG

WI- 21703c	134	A G ---			CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGAGGTGGTGGCTGGGCAGGGCTC TGATCCCTTTCCCTCAGCAGCAGACCATCTTACCCCTCGGGGAAGCAGCATTTGGAGCCTACACQ A/GJCTTGTCCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAG TGGCAGAGCAGCAGCTAGGGCAAGGACTTAAGGGAACCTTGTGGGGAAGAG
WI- 22663c	139	G A ---			CCCTTGTCAGTCTGTCCTGGCTCTCACTGCACTGGGAGGTGAGCGCGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACGTGGTGCACCTTACAG GC[G/A]GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTCTGAATCCGTGTTGAATGTGGGT
WI- 22663b	55	C T ---			CCCTTGTCAGTCTGTCCTGGCTTCTCACTGCACTGGGAGGTGAGCGCGCTC/GJGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACGTGGTGCACCTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTCTGAATCCGTGTTGAATGTGGGT
WI- 22663a	38	C T ---			CCCTTGTCAGTCTGTCCTGGCTTCTCACTGCACTGGGAGGTGAGCGCGCTCGCTAATCTTA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACGTGGTGCACCTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTCTGAATCCGTGTTGAATGTGGGT
WI-22668	99	A G ---			TCCTTTATCCTGCTGCCTGCCTGAGTATTCGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACTTAACAAATAGTTTCTGTAAATATT[G/JTCTAGTCCATTTAGATTGTGTAAATGATCTAA ATGNGTAAACCATTTAATACAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAAACTTTTATT
WI- 22631a	52	T C ---			AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTTCGAT/CJAGCACCATTTT CAAAGTTTAGGCAAGGTATTTAACCTCTCAGGCTCATTTCTCTTTGTAAAATTTGTATAATGGACC TATGTACCATCATAGGGTACTTTGGACAAATCAACTGAAATTTT
WI-20258	157	G T ---			AATCCACACTTTCACGGAGGGGAOCAGCCTGCCATGTGTCGCCAGGCTCACAGCAGCGGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATTTGGAACCCGTAAAGGCATGACAACG GGAGGCGCGGGGTGTTTCAG[G/J]CGCGTTGACGAGGTGCATGGCTGGCAGCGGCGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTTCCGGGGAAGTACC
WI-22714	212	C A ---			ACTACACATATGCTGATTTTCAACAGTAAATTAACATTTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTGTTTCCACTCTCTGCTAATCTGACAGGAGTGTGTGGGAACGAAGT CTGAAAAGGATTCAAAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAGGATGAGGTGAGCTT ACCAACCCCA[C/A]TGAGTAGGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44	G A ---			TGGGGCTACTTTAGATGGGATGGCGTCAAGGGTCTGGGAAGGCC[G/A]TCTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCGTGGAAGCCATAGTTGGATGGCGAGACTTTTCCGGCAGAGGAAT AGCAAGTGCAAAGGGCCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGGTGAAGGGCGCCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117	A G ---	---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCCTAGGAAGGAAGTGTTTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAACGTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTTGGGAAT
WI-22750	48	G A ---	---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTCTGACCATTCTGACTGTGCT
WI-22775a	60	A G ---	---	---	TGCTGTTCTTTAGTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTCTGTCTTTGAATCCCTTCAATCAGGCCAAA TATTTGTGAGCACCAAGGGCCAGATGGGAACTGAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143	C T ---	---	---	CTTTAGCTAATGAACCTGGCTATGTTGACTATGATAGACCAAGAAAGCTACCCAAAGTCTTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---	---	---	TCTCTGTGCTTGAGCCCTCATCCACCCCTCCAAAGCCCTCATGCCACCCACACCCGTGTCCACATT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCAAATTCOAAGGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGCGCTGTGGGTC CT[G/A]TTGGCGTGGTGATGTGGGGGCCAATCCTGAGGCCAGAGTTCA
WI-21031	31	C T ---	---	---	TTGAACACCTGACCTGACCTGTGACATGTGG[C/T]CTCTGGTCCCATTTGTCTCCAAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAAACACACACA
WI-21314	122	A T ---	---	---	CCATATCCAGTCTTCTTTGAAGCTTCTATTGACTTTTAGGTTCAAGTTATTATATCCTTTATCACTAT GACTTTCAATTTGATTTTTTATTGTTTCTTCCATTCTCTGTCAAACCTTTCT[A/T]TTTGTATTAA ACTGTTTTCTAAACTTCACTTAATTCTCTATCTGTATTNCTGTAGTCCCTGAACCTCTTTTAGAGG
WI-21186	95	G A ---	---	---	AGCGAGCATCAGAAATCACCTAGAGGGTTGACTAAACACAGACTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCCTAAGTGTGCAG ATGCTGCTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTCTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94	A G ---	---	---	CCACGATAACTATAAAAGCAGAAAAATTAGCTTTGAAAAATCAAAATACATATTAGTAACACACATT CATTTTATAAACACACATAAAGACACC[A/G]GNGTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTCATCACCTAGGGGAATGCTAAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	TTTTCCCATACCAATGCACCTGTTTGTATAACTATTTCTGTGGGTAAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTAATTAACAAATAATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTTATTGAGAAAGGAGAGTCAGCATAGTTATTTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAACCAACCAATGTACATATCTGATTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCTCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCAATTCGCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGAAGGAAA GAACTATTGCACAACCAACCAATGTACATATCTGATTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCTCCTCAGCAAGTC[G/T]GTCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCAATTCGCTCAGGAAGAA
WI-2117b	227 C T ---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACCTGAAATCTGTTGAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCCTCAAAATACATTCGGGG TCCAATCACATACCTCAGGTTCCAGACTCCTAGCTCCCAATATCTCAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTCTTCTACTGAATCTGGGTGGAG
WI-21122a	42 C T ---	---	TCACTTTGTATCATAATCCCTGTAAAGCTAAAGTTATTCATC/TJTTAACAGGAACCTGTTTTTCC TTATTCAAATGTCACAAGCCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACCTGGAAATACT AAACAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGTTGCT
WI-21254	53 A G ---	---	CAGTTTGTGTACAGGAAGGGCCCATGAATGTGGGGGGAACCTATCCACAGGAG[G/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	AAGGAACTGCATGGGTACAAAT[G/T]TCCAATTCATACTTAACAAGGTGGGGAACGGGTCAATTCT TGGCTGCTCCAGAACAGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGAAGAGACATATCTCACTGAAGTCATTTCTCTATTCT/GATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTAGGGTGACTATCCTTGCCCTAAT
WI-21059a	63 C T ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATATCTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTAGGGTGACTATCCTTGCCCTAAT

WI-20442	37	T C ---	---	TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	T C ---	---	GTGACAAAGAGGTGAAGCAAGGGGACAAGGGGCAGCAGGGCAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C ---	---	ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGGAATGCCTACATCTGGAATTT/CJCATTTAC ATCAACGTTAAATTTGTCCGACCAGTCTTCATTTGCTGATCACTTTTGATATATGACAGATCCAACAT GAAACTCCTGAAGCAAAATGAATATTTACCTTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTTGTACAGGGGATCTTCT
WI-21149a	167	G A ---	---	AGGACCTGCTCTCACACGTTCCCTCACCCACCAGCTTTTGGCAAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTTTTTTTAACAATGACCTTATTTATCTTTTAACTTTAACTGAGTCTTTATATA CAGACCTGCCAACTGGAAGCTTTTACAC/GATGCTTCAGAAATCGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTACCTG
WI-21376b	188	A G ---	---	GGTGTCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAGGAAAAACACTTTTCAATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCCGGAAGTGAGTTTCATGCTCCTCGGTGAACCA GACAGTGAATCTGTTCCAGCCCAAATCTGCAGCATTAGGGATGAGTTCTC/G/GAAGTGATTCT GAACTGAGCACGCACACTCATGTCTGCATGGGAACTCTGGGGAGAAAGACCT
WI-21382d	125	C G ---	---	CCATTGCAGTCCAGAGATGAGAAACTGGACCAGAGGCAATCATGAACAGAACGGGAGTCAAGAGA AGGGGTTCTAAGATGGAGAAAGTGGGGCGGTTTGGATCCAGTGGGATNTGGCTTCCQ/GJAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCACTGATGGGGAGCAGAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGTCGAGGAGAGCTGCTGCTCCATAGTCTGCGAC
WI-21437a	201	G A ---	---	TCCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAGAGGGACAAAGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCTTTGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCTGTGGGGCAGGAACATGCCAGGGCTGCTGGTAAATGGCAGGGTGCACTTTACCAGGGC/G /AJCAGGCATAGTGTGGCCCTGNCCTGGGCGCACCTGCGAACAGT
WI-21202b	156	A C ---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTTCTGTATAAGCTAAATATG/T/CJGA GTTTTATGAACATGATTTTATAAAAAATGGTCACAATATATTTTAACTTAAGTTAACTGATTTATGAGGG AGGAGGAGAGAGTTGACCAAJ/CJGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61	T C ---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAAATTTTATTTCTGTATAAGCTAAATATG/T/CJGA TCTGTTTTATGAACATGATTTTATAAAAAATGGTCACAATATATTTTAACTTAAGTTAACTGATTTATG GGGAGGAGGAGAGAGTTGACCAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	GCATGAAAGAACTCCAAATCAGACTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCATATGATATGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[AG]TCCAAAGTCATCTAATATTAACCCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTGCTTA
WI-21627a	106 A G ---	---	GCATGAAAGAACTCCAAATCAGACTTTATTCATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCT[AG]TTATGGATAITTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAACCCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTGTGCTTA
WI-21399a	75 C T ---	---	GGATTTAGTCCCACTTGATCTCAAATTCACCTTCTTGATGTAAACAAGCTCATTCCTCTAAAGTT TCAGTTT[C]TTTACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTTGCTTGGTAA CTGCCCTTGCAATTTGTCTGAGGTTGTGTGTCCTAGGACTAGGTAGGATCTCTTCTTCTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTTGT
WI-20329a	68 G A ---	---	CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGGTCACAGAGACAAGACATCAAT C[AG]TCTGTTAGCAGCGAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGGCTTCTTAAAAACAGTAAAAACCAATCAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATTCAAATGTACATGTAAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAAATCACAATGTATCTAAGTTTCACTTTTAAAGAACATTATAAAGGTAAT AAACTCTAGGTGTATCTTAT[C]ATGGAACACTAGTTTATTTCCNATTTAACTACTGTTTCATTCGCTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTAATAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAATTTGGGTC ATTTGAGAAACATTTTCAGACAAATTACAGTGGGGGCACGGCCGTTGGCTCCAGCTGGGTTTTCOC AGATGCAACAAT[C]TGGGGTTCTGGCTTCTCCACTGGTGGGATCGGCCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACCAGGAGGACAGCTGCTGGCAGGGAATAAACCCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACGCGGGCAGGGAGGGGAGAGAAAC[GA]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGATAGGTGGGCTCCAAACCCAGGCTTCTCACTTGTCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGGCTCTTTGGAGAAGGCA[AG]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCACCACCTATTTCTCCCTCCCTGAAG

WI-21475b	117 A T ---	---	TAGCCCTCTGCCAACATCTGGCAATNTGAGCGTGGGGTGAGCGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCJA/TJCTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGACGTGGCAGTGGCTTTTGAGAAAGGCAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCATATTTCTCCCTGAAG
WI-20893d	207 A G ---	---	TGTTTGTTTCCAGCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGAGGCTTGCTGCAGGG CTGCTCTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGTACAGTAAGTTTCATCCGCACTCC AGCGTCAGGCCAAACCTTTCGTTGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTCJA/G/ACATAACATTTGTAGAGTAACAACAACCAACCAAGCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTTTCCAGCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGAGGCTTGCTGCAGGG CTGCTCTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGTACAGTAAGTTTCATCCGCACTCC AGCGTCAGGCCAAACCTTTCGTTGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTTGGTAGAGTAACAACAACCAACCAAGCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCCCTTACCAGATAGGGACTAACTGGAGGGTGGAGGAAACAAGGTGAAA GGTATC/GJGGTCTGTGAGACAAAGCAGGGGGGCTGAGAACACAGAGCAAGGTGGTTTGGAG GGAGCACAGCAGGGTGCAGGAAGGGAGATGGGGGACATTTCTTATCCAGTGATGCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAAAGCAAGCG
WI-21552b	166 C A ---	---	TGGTACATGGACAGATGATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTATACCTTGATTATTTAAAATGTA/C/AJAATTAATTTATTGAATTTAGTTACCCCC ATTGTGCTATCAAAATATTCATCTTATTCATTTCTTTGTAACATTTATTGTA
WI-21552a	66 G A ---	---	TGGTACATGGACAGATGATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATACCTTGATTATTTAAAATGTAACAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATATTCATCTTATTCATTTCTTTGTAACATTTATTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGT/C/GJTAGAGAGGA AAGAGCTGGTGCCTGCTCTGGAGGCAACGTCCAGTCCGGGAAAGGCACTCGTGGTCTGTGATCTGTC TCAGTGATGGGAGGTCTOCACTCGCCCCACAGGCGAGCCTCGGGGCCAGAGATGAGATATGCTGTAA TCCAGTACAGGGGCTGCGTGGGGTCCCAACAGCTCTCTTTGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAGAGGATGAACCTGAAAACCTCTAAGGCAGGACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGATCTTTAAATTTATATTTCTCTTTAATAACTGTCAAAATACACCAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAGATAAAGAGGCGAGTGTAA[G/AJAGTAG TATTCTCTACATACCACAGTATACAATGATGCCTTCTCTGAGGTTTAGGAAC

-268-

WI- 21514b	133 C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGCJC /TACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANTTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---	---	ATGAAACATGTTGCAGTGGGATGAATC/GJTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTTACTGTATGAGGGTACTT
WI- 19576a	113 A G ---	---	TTTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAAACAAAAGTCACTGGCAATGATATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAAATTAAACATTG/GJTCTAGTTCAGTGATTAGT CACAGAANTTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA G
WI- 21695a	141 A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAGGCGAGTGGGCACCTTGGAAAGTGACTACACATGGCAATA AGCAGCCTATCTCTTTACCAACCAGAAAGTTCTTGGGCATGTGATGGTGGCAGACCCCTTCCAA GGGAATA/JCJTACTACACTAAGCCTACACTGTACTGTGAGATCATGGTGGAACAAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCCAGCAT
WI- 21574a	235 C T ---	---	AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACCTCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTAATGTCCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAACCTTACTGCCTACTTCCJTC/JTCTGTGAGGTGGGA
WI- 21644c	151 T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGGTCACTTAACTTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTCCACCATANTATTTAACAGACTCAAAGTGATACATAAAGCTTG TTTCATAAATAAGGGA/JJTCAATCAAGATCCATGGAATGATGCAGTTTAAACATGTGTCTCAGC TTGCCTACTGACCACCTTTCCTTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---	---	TGCTCTTAACCTCAAAAGTCCAAATAACATATAGACATTTTGANATAGCTATC/GAJTTTTAACA AACCTCAATTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAAACCAGTACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAAACATACGTGATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGCAGTTGGCTGTGTGTGGG
WI- 21615b	151 C T ---	---	GACCGAGAAAACACTGCAAGGCATATGATGTTTGTGGAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTTCATACATATAAGATAAGGATGGACT CTTCACTGAGTATTATC/TJAGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATCTATATTGGGCCAAAGGGAAAAGGTAGGATGGGTACTGTGGAACCGA

WI-21981	61	T A ---			TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAAT[A]GTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAGTACATGACAACATGCATGGGATAGACACTCTGTCTACAGATCCGTGCTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTTATTACTTTTTACATGTGGACAATCTAGTTAGGCGTTAAGGTTAAATTTGG
WI-21660	120	C T ---			TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAAACAGATACGGTGTAAACAGCCTCTCCACTGCTTACTGTGTACCAAGAAGGCAGAAAGCAGCTACCCAGCCTAACCTGGCC[C]/TTGTCTTTTTCAGGCTTCTCAGGATGCCACAGACATACTGGGAACTGGGATGAGGAGAGCCAGGGTCTGCTTCAGAGGGTACAGC
WI-19105c	211	C T ---			TGGAAGTAGCCCTCTGGACAGAAAGAAATATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTGTGTAGGTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCCAGTGGATCCTCCACAACTTC[C]/TTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCCG
WI-19105a	33	T C ---			TGGAAGTAGCCCTCTGGACAGAAAGAAATATTT[C]/GTGGTCCATGTGGTTGAGTCTGTTAAGAAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTGTGTAGGTTCCAGGGTGGGCACAGAGGTGAGGGCAGAAATTTGGGGTCCCAGTGGATCTCCCCAACTTCTCCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCCG
WI-21760c	81	C A ---			CAACCTAGTCACTCTACTGATGCAAAATGATTTGGAGGTGCTCTCCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCACCCCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35	A G ---			CAAACTAGTCACTCTACTGATGCAAAATGATTTGG[A]/G/GGTGTCTTCTAGCTTTACAATAAGNGGAGGGACCTCTGACTGCACCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198	T C ---			TCTGCCATATTGTTCCAGCACCACCTATTACTGTATTATTCTCTTTTGGAGGAAACCAGGNATTAAGAAATCTGGTTTGAATTTCCATGATGCCTAACTCTATGGTTAAAAATCCTTTTCTTACCACAAAAGGAACCTTAAATCACCAGAGAAACAGAGGGAGAACTGAGATATGTTGCAGAAATTTATCTCTACT[C]/AGAGACAATTCATAGTTCATAATCTTTCAGGGTTGTGCTTTACTTGGGGGGC
WI-20934a	72	T G ---			CCAACATGCAACATAGTCTTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAACATTTGTATTCAAGAAAT[G]/TCTAAGACAAATGGTCAAATATTCAAATGGCCTGGCAGTGTGGTAAATTCAGCAGACAAACAGCATGAGAAAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTTGCAATGAGTTACCCAATCAAGCCCTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTNTTCCACAGGAGA
WI-21561	55	T G ---			TTTCCATTTTATTACGCCGGCCATCAGAACAAATAGCATCTATACCTTCGAAACC[T]/GJCCTCTTAACCTCTCCAGGCAAGAAAGTGAATGATCATATTGAATTCCTCAGAAATGGTGGGATCTCAAGACTTTTAGAAAAGTGCTTATTAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCCTTTCTGGAATAATTTTGTGTAATCTGTTTAAAAAGATTTTGGATGCATGTCCCCA

WI-21961c	200 T G ---	---	---	AGCTTGCTTGAAATTTGGTACTTACTACCTTGCAATTCCTTATTATTATTATTACTTTTATTTTCCGTAAGTTATTGGGTACAGGAGTATTGGTTATAATAAGTCTTTAGTGGCGATTTGTGTGATTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGCTTTTATCCCTCGCCCCCT/GJC
WI-21961b	73 G A ---	---	---	TCCCACCTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTAATGCACTTTGCAATTCCTTATTATTATTATTACTTTTATTTAGCTTTGCAAAATTTGGTACTTACTACCTTTGCAATTCCTTATTATTATTATTACTTTTATTTTCC[G/A]TAAAGTTATTGGGTACAGGAGTATTGGTTATATAAGTCTTTTAGTGGCGATTTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGCTTTTATCCCTCGCCCCCTCTCCCACCTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTAATG
WI-21956	26 T G ---	---	---	CCCACCTGGGTCTCTTCAAGTGAAT/GJTTCCTTTGCTTCTAAAGCCCTTTAAATGAACCTTCCATTCCTGTTCTGAACTTGCCCTAGTCTGTTTCTGCTTCATGCCCCCTCAGTCGAATTCCTTCTCTGAGGCGGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTCCAGCCGGTAACCTCAGGGTAACCTCTATCTCTTCCACCGGTAAACAGAGGGGTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	---	CAACATACATTATGGCTGCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACAACATATTTTGTAGAACATGAGTGAGAGTGTTGTGTGTGCGCGCGCCGACGGCATGGCACTGAGGCGATTGCAATGGG[G/A]ACAGGATAAAAAGGTATAAAAACCTTGTCGCGAAATCTTTGCTTATTAAACCTTGGCCCTGCTCTCACAAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	---	TATAC TGTTT TTTGGTTACATGGATGAATGTCTAATGTGAAGTCTGAGATTTTAGTGATCCCATCCTGAGTAGTGATGATGTACCCAACTTGTAGGCTTTTATCCCTTACCTACCTTCCACCCCTCCCATTTTGAGTCT[G/C]CATAGTCCATTATATCACTCTGTATGCCCTTTGCATACCCATAGCTTAACCTCCC
WI-21139a	165 T C ---	---	---	GCCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGTTCAAGTCCCTGTTCTGCCACTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCTCTCTGTGAAATGGGTACAA
WI-20317b	217 G T ---	---	---	TGTGGGTCAAGCAGTAAAGGAACTAATACAT/GCTACAGCACTTCAGCACAAAGCCCTGGGCAACAGCACTGCATGGAAATACACAGGTAAACATTTTAAACAGTGGGACAAATTTTAAAGTACGTGGCCAGCTGTTGGTTGCTTGTTGGTCAATTAAGACAAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA
WI-22082e	179 G A ---	---	---	AATTTTGTTCTCTTCAGTTTTCATTAAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAA[G/T]TATTAAATTAATGCATATTTTGAGGCTACTCTCAGGACTTGTTGCTGCCAACTGCACATAAATGTCCTTTTGTGTTAGTATTGGTTGTGGGTTTCTCTTTTGATAGAATAATGTCCATTTAGTCCAGAGCTCTTGCTTTATCCGGATGACGGAGGGTACACGGGGCGTCCGCTCAGTCCCGCCGAAGGACGTATTC[G/A]CTGAACTGGGACGAGTCTACTCTC
WI-22082e	179 G A ---	---	---	CTCCCCACAGGAGGCCACGATTTCAAATGCTCTTTTGCTGCAACCTCT

-271-

WI-22082b	67 C T ---	---	CAGGACTTGTTGCTGCTCCCAACTGCACATAAATGTCCCTTTTGGTTGAGTTATGGTTGTGTG[C /TGTTCCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTCTGCTTATCCGGATGACGG AGGTACACGGGGCTCGCTCAGTCCCGCCGAAGGACGTATTCGCTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139 A G ---	---	AACACAAACTCCATGCTTTCAAGATCCACACCCAGATAGTAAAGACATATTAAATTTACAGCAAT TAAACAGGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCTGG GCTTCT/GJTAACAAGTGAGTATACATTAAAGACAGTATTCAGAAATGGCTTCAGGATTAATTTGA TTAATTTAGAGAGAGCCTATTTCAAGGCTTCCTAGCTCATCCACACATCACCC
WI-21723b	125 A G ---	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G]AJACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-22132	99 T G ---	---	CAACAGATGCTTGAGCCAAAAAGCAAAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCTTTTACTATCCTTT[G]CCTCATTTCTCTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCCTTCTAGTTAATGTCCTGCCCCAAACA ATACTAACCCATTGAAGGATACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---	---	TGACAGATCACACCACATTTGTTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTTTAAAGAACACATACACACATGTGCACACAC[G]AJAGAGGGCAAGTACAAAAATGTAACC CCACCAAAGTGATGTGAATGAAAGTGCAAAAGGCTTCATTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCCTGGCTTGGAAATAACTGAAAAGATTCA TTTCTCTTTGTGTACAAAGGATTCAAAAATATTTTCACATCTCTCTGCCAGTTAAACGTGCCGTGG CTC/GJCAATACACACCAAGCCAAAGCGTAACTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGTCACACTGTGTGCGCAAAATCAAGTTGT TTTAAATACAGGTGCGAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTGTTTACATAA CTCAGGCCACCTGAAATATCTGCTAGTGG[G]AJAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAAATAGGCAATGGGCAAT

-272-

WI-21079a	50 G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCACTGTGTG[A]ICGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTTGATTCTCCTCATGAAATTAAGCTGTGTGCTCACTGTGTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACTACACATCTGCCAGGTAATAGGCATGGGCAAT
WI-22129a	45 T G ---	---	TCTGTAGATTTTAGCCATGCCATATATTAACTTTAAGGAAAGT[G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAGTTAGCTTAACAGTTAACTTGAAGCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATTTGGTTGCAATTTCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC[A]GJGGATGAGGCTCTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCCTCACTGCATTGACCCACACCCACCTCACC CAGCACAGGCACACGCGAGGGCACACGACACAGNTGCACCTCACACGSC
WI-18916b	42 C T ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAG[C/T]GGCTTCCCACCTCTTGGTACCC GGTTAACTGOCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAG[C/G]CTCAGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCAAGAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCCAGNCTTCTGGCCCAATTCGGGTCTCCCCAAG CCCATGCTTCTTCCACTTCTCACAACTCTTTAGTCTTCTCTGACCCCTCACCACCCCAAAAT[A]G JCTTTTAATCTGGAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACCCCTGGCCCTGCCCT[C/T]AGCTGCATGCCACCCCTC ATATCCACCCCATCCAGCCTCCTGCCCGACACCCAGGCTCCCTGCTCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACCACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTGATTTTGCCATTACCCATAAATGGTGGGATCTACCTCCCCT CCTTGCAATTTGAGCTGGNCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19889b	80 C T ---	---	ACCCAGCTCCTTTACCCCTCTGGCTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGG[C/T]ACAGCAATTTATTTCCCTCTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTCTCTTGCCACAGTCGTAACTATTCG

WI-19891c	172 C G ---			TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATTCGTTGGTGCCCCCTCCCTCCCTCCCGG ACTCCTCTGTCTGGGAAACGTGGCTTGTCTCCAGACACGTGTGATGCCAGCTCTCCTCAGCGG AGCTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/C/GJGCTCTCCCGGGCGTGGGGCGTCTTGT CAGGCAGCGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---			GCACCTGTAGGGGTGTAGCTTCCATGGTTCTCCAAAGCACGGGCTGTACATACCTTAGGCTGACCAT TCCCTTGCGGGG[C/T]GCAAAACTGCTTTGAGGAAATNTCCCGAGGAGGAATAAACTAGAAAGACGC ACCTGCTATTTACCATCTATGAGAAATACAGCTAATGAAGTGGTGCAAGAACTTGGCCGTGTGA GTGCCCAAGGGTAAAGTCTCTCTTGTCTCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---			AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/T/GJACACCAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCCGCAGAGGGCTGGGAGGCGGNGGGTGGTGGAA
WI-20270a	53 G A ---			AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG/TATCAGTGATAC AATACATTCATGTCCAGGATAAGGAGCATAACACAGGATTTATACAGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCCGCAGAGGGCTGGGAGGCGGNGGGTGGTGGAA
WI-20622	130 T C ---			CCACTTTCAATATTTACAAAATGCTCAGGAGCAAAATATGAAAGCTTCAACACTTTCCCTTTGTA ACTTGTCTGCAATAAATGCAACTTTAACAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/C] TACTAAATTTTATGATGTTACTCATATTTTATTCATATACTTTTATGACATCATTTGCCAATACATA CATTATTTCTNTAACTTTATTTTACAATAAGCCCAACATCTGTATGCAG
WI-20768b	190 C T ---			TTCCCACTCAAAACTCCCACTCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTCTGTATATCACCACCTTA CAGGAGAGGTCTATTTCTGGGCACTCCAGAGNTCAGCACACATACTGCTGGGA/C/TJGAGGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---			TTCCCACTCAAAACTCCCACTCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC TCA/C/TJGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACCT CTACAGGAGAGGTCTATTTCTGGGCACTCCAGAGNTCAGCACACATACTGCTGGGAACAGGAGCTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---			TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAATATCTCATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTTGGTCATCTTTAAAGAAA TGCTTAAACATACCAAAGI/TJAGTGGAAATCAATAGATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCTAAATTTATTTCTATGTATGGAAAG

WI-22202	128	A G	---	---	---	TGTTGCTTTGGTTGTTGCTTCTGTGAAACATATTGGAACACTTGTTTTCATAAGCTGTCTCCTGACAGT GGCACATCCCATCCATCTTCAGGCCCTTTAATAAGGTCAATTATGAATCTGAATTTCTA/GJTAAAT ACTCTGGTGCAATTCATTCATCTGCAAAAGCAATGGCACAAACCCTCTGCCGGTGCAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70	C T	---	---	---	CCAAGGATGAAATTTCCACATTTATTTTNCITTTATGTGAATAGAAAATGGCAGTGAAGTGCCTATG AACTTGAGGCGAGGAATGGCATGGCGCTGCGGTACCGCTGGACGCTTGCTGTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109	T C	---	---	---	GGGAGGCATCATAGAAAAAACCCCTCAGCCAGAAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTGCAGGCTCTGGTTGT/CJTTCATTTGCAAAATAAAACCCCA GACCGGTCACTCTTCAGTTCCCTTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136	C T	---	---	---	GACGTACTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGCCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGGGTCAAGACCTTGCTTTT [C/JT]TCCAATCTCTCCTTCTAGCCAGAACTTTCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCCTTTCCCAAAATGTCTAAGGTCCCAATTCOCAGACCCCTCCACG
WI-22292	53	A G	---	---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA/WGJTTTGAGTAC GGTCGTTTAAAAAATCTTATCTGACCACAGTGGAAA
WI-22387	186	C T	---	---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCAACCAAAATGGGCAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACCTGGGTCTAGCATCCAGCCTCTCTCAGCAAGGACAGGATTGTGGT[C/J]CCTTGTGTTTCTG AACAGGGCCCGGGCAGCCAGGCATGCCATCACTGCAGCACTCAACCCCT
WI-22395b	127	A G	---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTCTTGAATATTTT GTAGGGATGGATGAATTGAAGTGAATTAAGTCAAGATAAGGGGGCAACTCTTTAAT[A/G]AAG GAAATGTTACCAAAATCCATAGTGAAGAGTAGAATATGTTCTTTAGAGTAGNTAGAAAAGTCCCCCAGG CTCCT
WI-22405	90	A C	---	---	---	TTTATGGCTCCTGAGTGCCCTTCAACCCAGCTACACTTTACCTTGATCTATAAAAGTGTAATTTAGAGT AAATACATTGGCTGTAAGTCG[C/J]GATCAGGTGCTCTCCACCACCAAGCAAAACAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67	T C	---	---	---	CCCTCTGGACAGTTTGTCTTATGTGTTGAGACAATCAAGNCTGCCCTCCAGGCACAGCCAGTGCTT /CJCTGGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTCACGAT
WI-21342d	59	T C	---	---	---	ATTTTCCCTTCTGTGTTTCGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGAIT/CJTGGA ATCTGCATGATTAATAACATTAAAGTTTCAAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTTAACCGAATGCAAAATTAGGTATCCCTCAAAATGACATTTCTCCTCCTAGTT T

WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCACAGATACITCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT[G]CAGACATTGCCTGTGCTTCTACCCACAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTTCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCACAGATACITCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT T[C]GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCACAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTGAGTCCCCAGTGGGTGCATCTTCCCTTATCTTGTGTTAAGCCACTTGGGTATACJ TCCATTCCAGCTCTGCACCTTCTCCAGTTCATGTGAGAGTCCCTGGAGGGAGGCTTCTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT[C]GAAAAAATACACAATGGGAACIGACA
WI-21965a	112 A G ---	---	CAGGTTCCACACAGAGGCTTTATTTACGCCACTCAGGACCTGGCTTTCTGCTCCAAGGCACCTGAACA CAGTCAGGCTCTCTAAACACTGGCAGGGACCTCCCCACAGCQ[G]CCCCACAGGGTCTCTGTT TCCCAAGTCTGATGGATTGAGGCAAGACCTTACACATTACCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTTCTTCCTAAG[C]GTGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAAGCGAGGGTTTAAAGGAGCCTGAGAAGAAATTCACAACATTTGACTATACAGAG TCTTCAATTCCAAAAACAGTTAATAGTAACCTTGGTGGCACATACAAATGCATTGAATACTCTGTAT TATTCAGTAACTAAA[T/C]AGGNTCCTGCATCATTTCTCTTCA
WI-22250b	132 C T ---	---	ACTTGCTTCAGGCAGGCACTTTCTGGATCTAAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTACATGATAGTGGGTTATTATGGGCTCTGCCTCCTGGCTGTGTTATG[C/I] GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGCTTCAGGCAGGCACTTTCTGGATCTAAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTACATG[A]TAGTGGGTTATTATGGGCTCTGCCTCCTGGCTGTGTTATG GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCAACACCTCCAGGCCAOCCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGAGACCCGCTGGCCCGAGGTTCTCGGGCTCTCAGGACGTCGCCAGCAAGTGA GCCACAGAGGTTTCTGGGACTCCAGCAGGGGATGAGGCCCGAGCCCAAGAACCTG[G/C]JAGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCCTGGGAGGTGAGGAAGGAGGT

UTR- 04932-2a	149 C T ---	---	GCAGCCATCCTCCTCTCCAAACACCTCCAGGCCACCCCTGGGGCCAGAGCACTCATGCCCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCGCTGGCCAGGTTCTCGGCTCTCAGGACGTCCAGCAAGTGGA GCCAGAGGTTTG[C]/TJGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTGGAGTGCTTC TTTGACGGGGCGCGTGCTCAGCTGCTCGGAGGTGAGGAAGGAGGT
stFIBBb	412 G C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACGCGCCTTGCACCTGCTCCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCAAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCCAGGAGCCTCTCTGA AGGACCACTGTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACGCGCCTTGCACCTGCTCCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCAAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCCAGGAGCCTCTCTGA AGGACCACTGTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stIGLV2	61 T C ---	---	GTCACAAAGGAGCGCTCTCGGACGTCTCCACCATGGCTGGGCTCTGCTCCTCACT/CJCTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGGTC TCCTGCTCCTCAGGCTACCGGGGCCAGCACTGACTCACTGGCATGT
stSG1001 7c	70 T C ---	---	GTTCAGGCTCATCTTGAACCTCCTGGTGCAAGCGATCCTCCACCTCGACCTCCAGGGTGTGGGAT TA/T/CJAGGCATGAGCCCCCAGCCTGGACACAAAATACATTATACTCTAAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33 G A ---	---	GTTCAGGCTCATCTTGAACCTCCTGGTGCAAGC/GJA/TCTCCACCTCCAGCTCCAGGGTGTGGG GATTATAGGCATGAGCCCCCAGCCTGGACACAAAATACATTATACTCTAAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63 A T ---	---	TAATGATAATTAGGGCATCTTCCACACGAAGATGACACAATTGACCCCAATATCATTGAGGC[JAT] AACAGTTTGGGCTGTTTTCCAGTAGTATGACAGTGA
stSG1009 6	36 G C ---	---	GTGAGAAAGATCGCTTTCTCCTCCCTCCCATGACCG[C]/JGGCTTCCCGGGGCACCTGTGCGTTTCC ACCCGAGACGGCCTTGTAGGGACCCACTGCCCACCTCGCTGCTGTGCGCTGGGTTCCGCTCCTAG GGCTCGAGTGTTAAG
stSG1011 8	107 C A ---	---	TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGAGGGCAGTACCCCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATTCCTTGG[C]/A/CTCAGCCCTCAGTTCCTTCATTCC ACGAGCCGTGCTGTTGAGTTTTCTCCCTCCAGTGAG
stSG1012 0	89 T C ---	---	TAGTAGGTAAGAAAAGCAAGGAGGATTGCTTATCGGATGACTGTTTACAGTGGTGTGACACTATGC CGTGTTCACGAACACTTTAATA/T/C/JGTTGTTGTAATCTGATTTTATCCTCGTCTTACAAATG
stSG1017 8	42 C T ---	---	TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG[C]/TGGGAGGAGAAGTGAACAGGAA TCGATCTTTGCTTTTAACTGCCCTTAGTAGGAGATGTTAAAATACTTGGC

stSG1019	3	136 G A ---	---	GGAACAATACTACCTAAGGACAAAAATACTATTATTAAAAAAAAGCTCTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTCTGTAGTGCCATCTATACAAACTTTTAC T[G/A]TTTGAAAACTGAGATTTAAGTTGCAAACT
stSG1020	2c	143 G T ---	---	AAGCTAACTTAGTGAATGGTGCCACTCAAAGGTCITTCGAGGGAAGCTCAGTCTGGCTTGGCGAG AGTCAGCCTTGGTCACCTCATAACGGGGCTCCAAGCTAAGCGGCTCAAGGAAGCAGTCCCAGCTCTCT CGCTGTCA[G/T]CAAGACCACAAAGGCAGATGCCCACTGCTGCCICTTTCCTTGTCTACTTTCT
stSG1020	9b	75 A G ---	---	TCTTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAAACTAAATCTCTTAAGATCCCCACTTTTAT TTTTA[G/G]CTCCAATAAATGTAATTCAGCTGCTGAAT
stSG1020	9a	34 C T ---	---	TCTTTTCTCTTTTCACTCTCAGTCACCATGATT[C/T]AAATAAACTAAATCTCTCTTAAGATCCCACCT TTATTTTAACTCCAATAAATGTAATTCAGCTGCTGAAT
stSG1021	8	29 T C ---	---	TACTAGACATGCAAAATGAGAAGATTACA[T/C]GTGAATATTTAAAGAAGTTATATTTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTAATCTGA
stSG1025	2	108 A C ---	---	ATAGGTTTCAGGAACAAAAATCATTAAATGGAATAATGAGAAGAAATCTTTATTTTGGACCAATTTT AGGCACTTAAGAGTTTCTTTTCTTCTCTTTCCCTTTGATCA[A/C]AGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915	0	123 A C ---	---	CTGTATTAAATTAAGAAAGGCACATAATGAGGGACGGAAAAATCTACCTGTACACAAAAATCTGTAC TTTAACAGCATCTTCAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG[A/C]ATTTTAA GAACTGAGTTATTGGAC
EST11023	1	166 T A ---	---	TTTTTTGTTAAACCAACCACTGAAAGTTCCACATGTGAAATATAGATACAACAGTGAACAAAAAT ATGTGGCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACAGCAGGGC AATTAGTCAATTAAAAAAAATAGTACATGTTAT[T/A]GTGTAATAAAATTAATTTACAAAAGGCTTT TCCACTCGTGGATTGTATCTCTTTTGGAGGAGGGAGTAATCCTGG
EST14096	8	71 G C ---	---	GGGATGTATATTACAGATAACACAACCTCACAAATATACCATCAGACATTGAAAACTAAGGCCATTCT GTGA[G/C]TTATTTTAAAGCTGGTGTTTGCACATAATGATCTTAAAAAAAATGAATTACCAAA ACCAAGATTCTCTTCTAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113	6c	125 C A ---	---	TGCAAAATTGTAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAATGTGAGGTGG CAGGGATGCTTAAAGTCTCCTCTGGCAGAGACCCGAGGTGCAGAGATGATCTTCTCA[C/A]CCCTTC TCTCAGGGTGTGGAG
EST22555	7	60 G A ---	---	TCAAGCATGTGTAAGGCACCTGCCCCGCCAGACCCCTTCTAACTTCTGCACACTGGAAGGT[G/A]AAA CCTGGGAGAGAGAAGACACTCCCTCCCTAGCTTCTACCTGGGACCCCTCCAAAGATGAGCATTCATC TTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

-278-

EST22917 6	74 C T ---	---	GTAAACCTTGCAAACGCCATGCTAAATGGAAGCCTGACTGACCGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/TTTGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGGAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACCTTAACCCCTCAGGCTGTCCCTACTCA/A GTTGGTTTGTAGCCTCACTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAGTCACCTCTCCA
EST36745 3	56 A G ---	---	GAGGGGAACTTCAAAGAGGATTCCAACAGTGAAGCAGAAATCATGGGGCAAAAGTC/A/GCTATGG GGCCAGACTGAGGTGGACCAACAGCAAGCTCCAAAGCTGGGCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGAGTAGCCAT
STS- R37410c	201 A T ---	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAAGAAAAATCCTCACTTAAAAAAACAAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGTATG T/A/TJTTATTTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAAGAAAAATCCTCA/C/TJTTAAAAAAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	TGTGACCATACCAAACCTATGCAATAAAGAAAAAGAAAAATCCTCA/C/TJTTAAAAAAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAAGTTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R42778	74 C T ---	---	TATCGTGGGAAGTTTCCAAACCTCATCTTATGCTGCTTTTCTACTTGTCTAATATTGGATGCTTCTTGCCA GGCTC/C/TJTTAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAAACCTGAA
UTR- 04350	125 C G ---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGGG ACTGCTAATCAGTATGGGTTTCTCCCGGATGGTGAATAATGTTCCGGACCTAGATA/C/GTGAACGA AGGTAGCACGACACTGTGAGTGCACTAA
stSG1026 6	55 T C ---	---	GAAATAAACTAAACTGCAAAGCAAATCACTGTTAATAAGAAATTGTTCTTCTGT/T/C/GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1028 2	70 T G ---	---	GTATAATTCAGCATAAGCCAAAGCCTTTTAAAAAACCATACTATCATTTTATGAAATCTTTTACA AGA/T/GAAGCACAGTAGTACAAATATTTAAGCATCTCAAGCTCCATTTAAGAGTTGACTATC
stSG1031 0	128 C A ---	---	CACCTTAGATATGAGGAAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGTATGCAATAACAGCAATAATTTTTTCACT/C/AJTTG TCAATGCCAATGCATTGAAAGGCCCAAGAAATGAGAAAAGGATAACAAACCTTTTGATAAAAAAGGTA AGAAATTTCTGTGTG

stSG1033	116 T C ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGGATGCATTTTCGG GCTCCAACTGTCTAGGAAGCCTAGACCTCAACACCAACCTCCATTC/GCATTTCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTCTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
1b				TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGGATGCATTTTCGG GCTCCAACTGTCTAGGAAGCCTAGACCTCAACACCAATTCACCTCCATGCATTTTCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTCTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1033	107 A T ---			ATTGGCAAATGGGAAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAATCCTCCTCTTG AAATTATGTCAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTGTC[G/A]AAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGGTTGAGGAGCGAGGAGGAGTTATTT TGGTGGAATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT/GTCAATCATTAAGAA GACAAAGGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTGTCG TCGTCCTCTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT TT/GCTTTTGAGCACCTTGCCACTCTGGCTGGTCTGCCACTGATTGTGACTGTCTTGTGCTCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTCCAGTTTGGCTTCTGTCTCTCAT/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTTAGGTCC[G/GCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTCTTTAATCAAAAGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCTTAGTTCTGCAGATGGGTA CACACCCACAAGTTTCAATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCCAGTGTGCA TC/GJAAATGTGGAGGATGTCTGTGTCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAAAGAGAA AATGCCTGA
1a				ATTGGCAAATGGGAAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAATCCTCCTCTTG AAATTATGTCAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTGTC[G/A]AAAGTATTTTCAGACCAAAAAGGAGGT AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGGTTGAGGAGCGAGGAGGAGTTATTT TGGTGGAATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT/GTCAATCATTAAGAA GACAAAGGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTGTCG TCGTCCTCTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT TT/GCTTTTGAGCACCTTGCCACTCTGGCTGGTCTGCCACTGATTGTGACTGTCTTGTGCTCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTCCAGTTTGGCTTCTGTCTCTCAT/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTTAGGTCC[G/GCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTCTTTAATCAAAAGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCTTAGTTCTGCAGATGGGTA CACACCCACAAGTTTCAATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCCAGTGTGCA TC/GJAAATGTGGAGGATGTCTGTGTCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAAAGAGAA AATGCCTGA
stSG1243	225 GA ---			AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGGTTGAGGAGCGAGGAGGAGTTATTT TGGTGGAATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT/GTCAATCATTAAGAA GACAAAGGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTGTCG TCGTCCTCTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT TT/GCTTTTGAGCACCTTGCCACTCTGGCTGGTCTGCCACTGATTGTGACTGTCTTGTGCTCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTCCAGTTTGGCTTCTGTCTCTCAT/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTTAGGTCC[G/GCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTCTTTAATCAAAAGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCTTAGTTCTGCAGATGGGTA CACACCCACAAGTTTCAATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCCAGTGTGCA TC/GJAAATGTGGAGGATGTCTGTGTCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAAAGAGAA AATGCCTGA
b				AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGGTTGAGGAGCGAGGAGGAGTTATTT TGGTGGAATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT/GTCAATCATTAAGAA GACAAAGGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTGTCG TCGTCCTCTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT TT/GCTTTTGAGCACCTTGCCACTCTGGCTGGTCTGCCACTGATTGTGACTGTCTTGTGCTCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTCCAGTTTGGCTTCTGTCTCTCAT/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTTAGGTCC>G/GCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTCTTTAATCAAAAGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCTTAGTTCTGCAGATGGGTA CACACCCACAAGTTTCAATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCCAGTGTGCA TC/GJAAATGTGGAGGATGTCTGTGTCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAAAGAGAA AATGCCTGA
stSG1345	60 GA ---			AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGCAAGTATCTCTGTCATAAATTTGAAGTATGTTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGGAGGGGCCAGGATGGAGGGGTTGAGGAGCGAGGAGGAGTTATTT TGGTGGAATTCACCACTTTCCCATGAAGAGGGGAGACTTGGTATTTTGT/GTCAATCATTAAGAA GACAAAGGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTGTCG TCGTCCTCTTCCAGTCTTCTGCCAGAAGCATCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT TT/GCTTTTGAGCACCTTGCCACTCTGGCTGGTCTGCCACTGATTGTGACTGTCTTGTGCTCC GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCTCCACTCCAGTTTGGCTTCTGTCTCTCAT/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTTAGGTCC>G/GCTCCCTTGCATGA AATGTGGGAGAGGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAGTTCTTTAATCAAAAGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAAATGCTTTCTTAGTTCTGCAGATGGGTA

stSG1847 b	95 G A ---			TTGCAGACAACAATGGAAGCTTTAAAGCTCTTCAACACAAAATGCTACCCCTAAATGAAAGAAATTT AGAGGTTAAATAAACAAAGTGAGAGACC[G/A]TTTACTTACATCAGTTGCGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTTCCAATGTGAAACCAAAATTAATAAATGATGATCAGTGTGCT TCAAACACAACG
stSG1847 a	49 C A ---			TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAAATGCTACCC[G/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAACAAAGTGAGAGACCGTTTACTTACATCAGTTGCGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTTCCAATGTGAAACCAAAATTAATAAATGATGATCAGTGTGCT TTCAAACACAACG
stSG1897 a	83 A G ---			CTTAATGCCCTTCTCTCTCTGTCACAGGAGACACAGATGGGTAAACATAGAGGATGGGAAGTGG AGGAGGACACAGGACT[G/G]GCCACCACTTCTCTCCCGGTCTCCCAAGATGACT
stSG2022 a	86 T C ---			TGCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATACAT[C/G]ATTCATAATCTCATCTATTTAACATTAAACACAGGCTTTGTTGT TGTTATTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---			AAACGTTGTCCCAAAATTGTTTCAGTTTCAAGTATAAAATAAGACTTCTGAAAAAAAAGTTTACA ATTAGTTATAAAACACCTTAAGAATATATTTGACATT[C/G]ACATCACAGTGGGCAATTTT
stSG2108 c	71 A G ---			TTGAGCAACAATGATTGCGAATTGGGCACTCCAAACCAAAAATGATT[C/G]AGGGGCTCCACAGAG GAGC[A/G]TAAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---			TTGAGCAACAATGATTGCGAATTGGGCACTCCAAACCAAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCCTGCGATGGCGATGGTGCAGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTGTTGCTCTG
stSG2141 a	113 C T ---			TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTATTTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCCTGCGATGGCGATGGTGCAGGTG GGTGCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAGTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTGTTGCTCTG

-281-

stSG2148	50 A G ---	---	TGGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTTC/GJAAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGTTTATATGGCAGATGAGCTGTACAAATCTGTTGTGTGCT [C/T]GCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGGCAGAGGAGGAGTGAAGGACCA
stSG2189	41 C T ---	---	CAAGTGGTGAAGCTGGGATTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACATCATCGCTAACTTTGAGCACTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGGTCTGTATGATG[T/C]TTTATATTTATGTAT AATGCTTACCTGATGATACCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTCTGCCTCTGCTTCCCAGTACTACCCCGTCCAGCAACGCTCCTCGTATAAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGTCTAACTCTGTGAGGCAGGCTATCAGAAAGGGCAG[A/ C]CTGCAGGAACTCTCGCCAAAGCACTGGGCTGCTCCTCAGGCAGAAATTTCTCCT
stSG2306	67 A G ---	---	GTCATCAGCGTAGAGGTCAGTGGTATATAACAAACAGTAGCTATATGATATTTGGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAAACCATGAGGTGAACACTTTCACCTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAGAGAGATGAAAGAAAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGGGGCTGTGGGAGGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAATGTTGAATCAACAGACCTCAAAATGCTTGACTGCAGAAGTAACTGCTGTCAC[T/C] GTTCTCAGAGTCACCATTAACGGTGAAGTGTCTATTCTGGCTGTCTTCTATTCATCA
stSG2465	76 C T ---	---	CAAGACTAAGAAAGCCGCCACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCCTC ATCTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTTGATTCCACAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAAAACCAA GATATATAAAATATTGAAGTCATTTATGCCCTTTTGATGACTGGTTAAATATGCAAAAGCAGCTAAAG GAATA[T/C]TACACCACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGGAAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTCAGTTTGGT CCCAATATAGGCCCTTCGCAAGAAAGAGATCAATGCCGAACCGAAGTGTGAAAGCA[T/G]GAACAATC CCGGCCAGATTAAATTAT

stSG2577 a	121 C T ---			AATTGCCAAATGGAAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTCATCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[C/T]ATGAACAATC CCGGCCAGATTAAATTAT
stSG2700	58 G A ---			ATCTCTGACTGCTTTAGTGGGAAAGGAATCAATTTATTAAGAACTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTGGGGAAATAAACCACTGGTCCAGAGCAGAGGAAGGCTACTTGAGCCGGACACCA
stSG2724 b	101 T G ---			AAACAAGCTTTGTCATTTCCACTACATTTTGTGTCTTTTATTAATATTTGCAATGCTATAAT TTAATACTTATATCCAAATTGCTTGCCATAATCA[T/G]TTTTTTTATCCTGGGGTGTGAAAGAAC
stSG2776 a	65 G A ---			GTGGCCGATCTTTACTTTCCAGAAAAGCGGTAAATAAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATGGCCCTTTTGGAGTTAGGCCAGGAACCTCAAAACAAGGGACACTGCTGGCCAAOCCACAAA ATATCCACTAATCCCGAATATAGTAACCCCTGTCTTGCCGAATG
stSG2791 b	109 G T ---			AAGGAAAGGTGGAGGGAAGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAAACTAGCAATTTTAAATAATTT[G/T]GGTCCACTTAAATCTATTA AAGCAGAAAGGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2791 a	100 A G ---			AAGGAAAGGTGGAGGGAAGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAAACTAGCAATTTTAAATAATTTAGTAAATTTGGGTCCACTTAAATCTATTA AAGCAGAAAGGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2826	85 C T ---			CCGCAATTTCAACACACATTCATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAACAA[C/T]GAACAAAATAAAGAAAACCCCATGAAATGCCCAGGTTTA ATTTTTTTCC
stSG2850	88 G A ---			ATGGGTGCATTGTAAAAGGCAAAATTAATACTTTTCAGGCAGGGGTGGCAAAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAAATACTCCTCCCAT
stSG3031	71 T C ---			ATACTCACGGGGGCTGAAGGGCAATGTGAAGAGTGACTGCAAGTCTCTGGCATTTTCTGTGGTGCAGC AAAT[C/G]GCCCTTTATTTTAAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81 G A ---			GTCCCAACTCCTCCTCTTAGAGAAAAAACTGTGATTACCTCACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAAAGCATCAAAAGCCAAAAGGCAAAACTGGCTGAGGC
stSG3092	94 T G ---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTGTCACTATTGAAAAACAAGCCAAAGTTC CAAAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATTCCTTATGGTCCAGCCCCCTACTTT AGTT
stSG3230	95 A G ---			AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTTGTCAGTGGAGTC[A/G]GTGGGGTGTGAAGTGTCTGAACCTGAAGTAG
stSG3245	160 G C ---			ACATCTCATACCCAGTAGATGAAGAAAGGAATATCTGAGCAAGAGCCCTGCTCCAGGGGCC CAGGTATGTGAGAGGCCCAAGTGGGGTGGCCACTTGGTGTTCACACCCCCCTGCCAGTCTG GCCCCAGTACCTACCTGGGAGGTTG[C/G]GTACTTGGCTTAAGTACTTCATGCTTTAT

stSG3265	42 T C ---			AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAAT/G/CACATTTGTAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTTTCAGCCACACATTCAGTGTATGTTCTAAATAACACATCGAC AGGACTGTCTGTTCAAGTACAAATGGAGGACAGCTTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTGTGAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141 C T ---			TGTACTTACTGTGTCATCCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/T/TGTAGATCCCCAAGTCCCTGACACATTTTCTCTAAGAACT
stSG3269 a	24 A G ---			TGTACTTACTGTGTCATCCTATCC/A/GJTTCCCTCCCTGAGCCTGGACTGCTCTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCCAAGTCCCTGACACATTTTCTCTAAGAACT
stSG3284	130 C T ---			TTAACTCAAGAACTTTTCAAGTACAGGAAGATTTATCTAATATTAATAATGACTAAATTACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTAAATTGCTGTAAATGGGACATTTGTTGTTTGTATCTACCC
stSG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAATATCTAA/JTJACAAATCAAAATAGCATTTTCTTAACCTCAA TAAATGTCATATCTTTAGCTCTACT/C/AJCCAGTGTATCCATTTTCCCAAGCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCTGTCTGGACATTTGATATAAATGAGTTGCTGTATCATGTTGAGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGCTTCATTCCTTTAA GATCCCCAGTATTATTTCTAAATTGAACCTGTTTGTGGAAATAAAAAATCTGAGGACCACCTCAGAG GG[C/T]ATAAGGGAACCTCTTTGTCTTAGTTTCATAAGGACTTTCT
stSG3369	69 C T ---			CAAGACTGTAAAGACGTAGGCTTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAAGGAATGACATTTCCAAACTGTACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3398	125 G T ---			TCCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG/A/GJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3416 a	43 A G ---			GTAAGACAAAGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCGCCGACTTTTAAACTGAAT GTTGAAAATCATTCTGCTTTGCTGGTAAACACTGA/T/AJCAAGTTGCTTAACTTTGTGAAACCCAC TTTCCCTATCTGTAACAAAATGGACAAACAGAACTTTTCTCTTCTCTC
stSG3424	173 T A ---			GTTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTCAGGTTGATGTGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGGCCCTT/AJGAAATAGCTTACTCTGTTTCTCTAIC
stSG3436	88 T A ---			

stSG3463	103 C T ---	---	GATACAGAGATAGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTCAC[C]/TJGGAAACAAACTTGCTTGACTATATTA CTGA
stSG3491 b	71 G A ---	---	CAAGATACCTTCATTGTCTCTAAGTAGTGCAGTCTGGCAAAATATTTCTCACGAACAAGGACGATTTG AAG[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTCTAATCTTTACTGGCACCTGTGGATTCTATTAACTCATTTATACTATTTCTGTGATG ACAGAAAAATAAGTTAAC
stSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTT[A/C]TGCATATATGTGTGTACAAACACACACACACACC CCTAATCCTCAAAATGCTCTGGCATAAGTTTATCTCTACTGGTCTC
stSG3536	213 A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCACTTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAG[A/G]TCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
stSG3583	112 G A ---	---	GAAAAAGCTTAACATACGATCCATGTGCAAAACCCCAACAGGATCTACGAACCTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]AACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGT[G/C]JACG CCTGTAGTCCCTACTTGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGCCATTGCCACTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101 T C ---	---	ATATAGTCTGGTAGCATTATAAACTCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATAGCACCCCTGGCACAAAAACCCCAATGAT[C/J]CTATTCCAAAGATGTATCCAGATGAAA GTATCCAACAACAACAAAAGCTATATACAC
stSG3590 a	70 A T ---	---	GAGAGATGAGCTATTTATCTTTTAAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AAA[A/T]TCTCTGATGCTCTTGACCCCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTT[A/C]AACAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	ACATATGTAACCTGCCATTAGTAGCCATATTTAGGATGAGAT[C/J]GGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAAATAATAAGTTAICTGGGGAACGGCCATTTGTCCAACATTACTAA GTGCGCTACTA
stSG3646 c	70 G A ---	---	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATTAACTTTGATACCTTGTTAAGATGGTGTCTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA/A/G/TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG/A/TJTGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---			ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAAACCCTGGACTCACCT GAAATATCCTACGAGGC/A/C/JTCGCCCTCCGAGACTGACGATTATTAACCACCCACACGGAAAAAGG
stSG3693 a	30 C T ---			ATTGTTTCCCTGAACATTCCCGTGGTCTCC/C/TJCTGAAAGCCGATGACCATCCAAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAACCACCCACACGGAAAAAGG
stSG3698 b	145 G A ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG/G/AJAGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---			TCCTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTTG/C/JTCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---			ACCAGCTCATGTGCAGAGGGTCTCTGCTGGATCCCCAACTGGAGCCATCCCTGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGATGTGAAG/C/TJACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---			GCCAAAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATACCAGCCCAACAGCAACAGCCCG/G/AJAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128 G A ---			CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---			TTCTGTGCAAAAGAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT/AJAAAGTTCCCTAAGA CACTGAGGGCATAAACCACCAAAATAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115 G C ---			GACAAAGGGAAGAGATGCCAGAGACAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCCAGGGC CACCACAGTCTGTGGGTCAAGGCCCTCTCTGCGGAGCAGGTTCTA/G/CJGGCACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTCTGCCCCT

stSG3880 a	36 G C ---			GACAAAGGGAAGAGATGCGCCAGAGACCAGGGCTG[G/C]GGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACACACAGTCTGTGGGTCAAGGCCCCTCTCTGGGAGCAGGTCTAGGCACGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT
stSG3895	44 A G ---			AATCAGCCATTGTACACATTGCAGCTATGATTGTTAGTGTG[G/G]TTTTTTTCCATTAACTAA TACATGCCCCATAGATATATTCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
stSG3902	104 T C ---			TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCACTATTTCACCTAAATGTGAACCTGCTTTCTTTTC[T/C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---			GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
stSG40	25 A G ---			GAGGAAGAGGTTGAAGAAAGTGTGA[G/A]AAATATATTTAAGATTTCTTGGGGAGAAATCTCGTGC CCAAACCTGTGATGGATCCCTTACTATTAGAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCAA
stSG4009	32 A G ---			GTGTGGGCTGTGATGATGAATGGCGCGCT[G/G]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATTTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCACACTGCTTACA
stSG4033	123 T C ---			AGAAAGCTTGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAACCTACAGTGCAGTAACCAAAAGAACCTAATGTTTTCAAGCATAAAGGTACTTTT[C/T]GTGAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---			GCTGAGAGCACGTGTACAGCACCGCTGT[G/A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTTCAGGCTCCCGGAGAGCACTGAGGGTTCCATCACT
stSG406	53 T C ---			ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAACGCAACAAA[T/C]GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTTCCCTAACAGAGATTATTAACTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 G T ---			ATCTGGGCTGAATTAGTCAAGCAGGT[C/A/C]GATACTATTGCTGCTAGATGTATTAG[G/T]ATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGGCCCTTCATCCTGG
stSG4095 a	27 A C ---			ATCTGGGCTGAATTAGTCAAGCAGGT[C/A/C]GATACTATTGCTGCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGGCCCTTCATCCTGG
stSG4120	65 G A ---			TGCATGTTCCACATCTTTTATAACAGCAAAATGTATAATAAACTACGTACTTATGGATAATCAC[G/ A]CTTTTCCCTCAGAGAGCCCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---	---	CTTGGCAGATAAGGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTCT[AG]TATATTATTT TACTTCTTGAAATGCCACATAATTTGCAATAATGATTCACCTCCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTC[GA]GC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG[A]CAGGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGACCACGGAGGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACCAGAGC[GA]CCACGGCCGGGACTCCCGCGATGGCTGGGGG GCTATGGCTGTGACAAGAGATGAGCGAGGGCCGGGGCTGCTCCTCCCCAGGGGCGAGACGTGAC TGGGGGACCATTGGCCGAAGAGAGGATGACCGGTCTATG
stSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGTAGTGGCTCCACACTTTCCAT TTAAGCAAAATAAAT[GA]GCTTCTGAGTAGTGTCCAGTTTACCCCAACATTTTG
stSG4331 b	71 T G ---	---	CTCACAAGGGCCACACAGAAAAGATACAAATACATTATCCAGCTAATATTAGTTTATGACAC AGAGT[GT]TTTCAAACAAGTTTAAGTGTCACTGAAAGAGCATGTTAAAAAGTTTAAGTTATCATT GGAGAGCAGATTCTTGGCTCGCCCTTGATTTCTGAGGGGTGTC
stSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[GA]TAAGTGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	TTCCCAACCATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGTTTGCATGACTCAAAATAGGCAC AAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGC[A/C]CCTTCACAAC TAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTGAGG
stSG4361 a	24 T C ---	---	TTCCCAACCATTGAGTGACAGAGCT[CA]CAGTCATGCAGAACTCAGTTTGCATGACTCAAAATAGG CACAAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAAC TAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTGAGG
stSG4376	73 A G ---	---	TTTCACTGCTACTGTTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTCTTCTCCAAGGGGAG AACAG[AG]CTGGAAGTGGGCTCTGCAAGAGCCATTCTTCCAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGATGACAACATACGATTTTCTTT[CA]CAGTCTTGTAGT ATCCACAGTAGTGTCTGTCTCCATGTACAAGTGTCTGTCAGAACACCCATTAAATTCATGCC
stSG4410	79 A G ---	---	ACCAATGGTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAACTAGTCAAGGGCTTAACCAT TCAACACCCGC[AG]TGACAAACGAAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65 C T ---	---	AGCAGATCAGTCAGCCACCTTGCTCTCTCTTTAGGGAGAGGCTAGGAGTGAACACATCA/C/
stSG4430 a	54 A G ---	---	TJGTATGCAATGAGAAAAATAACCAACTGGTAGGATGGGAGGGGAGGCAATAGGCAC
stSG4448	99 G A ---	---	AAATGGAATTCATCTGGCTGTCTCTCAGTTC
stSG4449	92 T C ---	---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACCTTTAGTAGTTCTATAAGGTJA/GJATTAAACATA
stSG4467	42 C A ---	---	GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCCATTTT
stSG4475	21 A C ---	---	CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCGCCCAACCCAGGCTCT
stSG4477	32 A G ---	---	CGCTAGCCCTGCCCTCTGGGTCACTGC/GJATGGGTTAGGCCCCCAAAAA
stSG4531	79 C T ---	---	ATTAGCCATTCACTTTCGAACAATTGCTTTACTGTAACTAAGTACTGTACTGATGATGTTTACAAT
stSG4550 b	86 G A ---	---	TAACTTTGGACAACCTTAAACCTTA/CJTAGTGACATTTGCTGTCTATAATAATCAATACTTCATCATA
stSG4550 a	85 C G ---	---	GGCTGAACATAATTATTAAGAAGCAAAAGTTACCCCTCCC
stSG4590	47 A G ---	---	CAGACATGAGGATGGCCCTGTCTCTCTGGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTTGTGT
stSG4623	22 T C ---	---	GAATGAAACTCAAACACTCTTCAGTTTTTAGAGTCACTTTCTGGTATCGAGCGACCACACCGAGGAG
stSG4843	102 A C ---	---	CACACCTGCTTCCAAAGGCTGCTGCTTCTGCACACAGT
		---	ACATGTCACTTCTGACCAGGJA/CJTATTAATAAGTTTATTTAGAGAAATGAGTTGAAGTGAGCGGA
		---	TTAAGAGACACAAACTGGACTTTTGTCTTTCTTTACTGTAGCACCCAGGTTTCATG
		---	GTAACTTCTGGGGTGGGGTGAGACAAACA/JGJATGAACCAATAATTAATTACAATTATACATT
		---	TCAAGGAGACTTTTAACTAGGTTAATGTGAACGCGAGCCATCAATGGTTTGTGAGGAAAAAGGAGA
		---	TGAAGTCTGCTCTGGGGCAACGTTTGGCTCTATTGCGAGTCAGACTTGGC
		---	TGAACTCAGAGCTGGTGGGAGCTGCAGCGAGGGAGGCTGGGGCCAGATGAGCCGCCGGGA
		---	CAGCAGGCTG/CJTGCCAGCTCTGGCTGGTGGTAGAAGAGGACATAGGCTGCCTTGGACTCGATCT
		---	GATTCTCATTGACAGGGGAGACGCTGTTGTCATCAA
		---	TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAAACAGGCTTGATGAGGACAGAGTCTATT
		---	AAAAGAGACAGTGGGCAC/CJGJCAATTTGAGGGGAAGGGGGGCGAGGTTTTAGAGAAC
		---	TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGCTTGATGAGGACAGAGTCTATT
		---	AAAAGAGACAGTGGGCAC/CJGJCAATTTGAGGGGAAGGGGGGCGAGGTTTTAGAGAAC
		---	AATCAGGCACAAGCTCGGGAGAGAAGCCCAAAAAAGCTCTCTGCAC/JGJATGGGAGGGAGACAC
		---	CATTGAAAAGGCATCGTTCTTCTTCATGCAAGCGAGGCTGGCTCCCAACAGGCATGGTCTCTTG
		---	AATCTGTATCACCCAGCGCTGG/JCJCAATGTACTAGTAGCTTTCCACAGGGATTTTTTATACTATTC
		---	CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTTCACATTATCT
		---	TAATATCTCTTCAAGATGCTCTGGAG
		---	TAAAAAAAACAACCCCCCAAAAAACACCCAGAAGTTTTTGTGTTTTATGTTTTTCAGATTTTAAAG
		---	GTATTTTCTTCTTAGCTTCTAAATTTTGAGTCAT/JCJATCAGAAAAGTCTCCCTACTCCTCAAGGTGA
		---	GAAAGGA

stSG4850	38 C T ---	---	GGAACTCTAAACTGGGAATGGCCGAGGAGGAAGGGCTC/TGTGCACTTGCAGGCCACGTCAGGAG AGCAGCGGTGCTGTGCGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGCACAC TTGGTGGATTCTTGGGTCC
stSG4879	86 A G ---	---	AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTTTCTGTGAGGTCTGCTTTTGCAATGGCCTG CCCTGGGACTGGAGCAG/GCTTGGTGAGCTCTAGGTGGAGGGTGGTGGGAGGGGCATAGAAT AAACCTTCC
stSG4885	104 G A ---	---	ACTGGACTGGCTCGTTGCTGAGCCGGCTAGCGCGGTGGGACTCGGGTGACCACTGCTCTTCAG AGACTGCCCGCCGGTGACCACGACTACGCTCTGCC[G/A]GTGGGAAAGCAGAAGCAGGACC
stSG4896	112 C T ---	---	AAACAAATCAACCCCAATCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCCTCTGCCATAGAGA GGTTGGGGGACGTGAGGAGTGGTGGGGCTGGCACTTTCTCTAGCCACAGGCCCTTGAGG AATTAATTGACTG
stSG4932	22 G A ---	---	ACAGTGCCGATGGTTACACAATG/AJTGTAAATGTATTTAATCCCACTTACGAATGATTTAAATGA TAAATCTTATGTTTATTTTCATCACTACCAAAAGCGTGTGGTGCAAGGGTGTCTGTTTCTGGTCT
stSG4950	24 A G ---	---	TCATGACTCCCAGGAAAGGTCTT[G/J]CTTAGCTTCTCTCCCTACTTTCTCTACATGGTCAAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	AGATACGGGCAAAACACTGGGATGGCTTCCGTGACAACCTAAGAGGCTCCGAGTTATATTCTGGGT GGGAAACACTGACCCAGCCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC[G/A]GTGACACAGATGGGGCCCCTGCTCTATATCAAC
stSG4961	91 C T ---	---	GAAGTGTCTGTAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAGTA/C/TJAGAGAGGGCATTAGGCCAAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	ACTGGTGCCTCTCAGCAGATTCAGGGGTGTCGAGGGCTGGTTACCCAAACTCAGTAGGAGTGCAA GGGCT/GJTACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTCTCCCTTTCTTGCTGTGC AACCTTG
stSG4997	22 T C ---	---	CAAGGAGAGTAGGAGCCCCAA/T/CJTJTTAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATACACATGTTTAGAAGGGAGGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T ---	---	ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAAAC/A/CJTJATGCGATGCGGGAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345	107 G A ---	---	GCTCTGGTCAAGCAAAATCTCCAGGACAGAACAGGACAGTAACACACATGTATGACCCCTTA CAAGTGTCTTAAAGATTTTAAAAATGTGATGTTTTGTCCAC[G/A]ATAGTTTCAAGCAATTAAGAAAT GCAACCCAGAGAAATTCGTGAAAAACATTTTGCTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

stSG6362	88 G C ---				<p>TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAGGTTTAGCAGGAGC CTCCAATGAGCACGTGTATGTA[G/C]JAGAAAAGGAAAGGAGCAGGAGGAGGAACACAGATCTGCACAGA AT</p>
stSG8010	62 G T ---				<p>CACATCTGTGTTTTCTGGAGCAAAAGGGAACCCACAGAAAGGCCAGGAGTTTGGGTGTGCACCTGG[G/T]T GTCITTTCAACTGGGTGGAAACCAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAAGAATAAGA TGGCTT</p>
stSG8022	53 G A ---				<p>AGCTCCTGACTCCCTGTTACGTGACGTGATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGGTTAT TTACACCATGGAAACTGGAAACTCTACAAATCAATGCGTTTATTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC</p>
stSG8032	67 G C ---				<p>TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAAATTACTTCCAAAGAAATTCAGAAAAATTTGTGTGT GCTGGGAGGCAGGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA</p>
stSG8064 b	46 C A ---				<p>AGCTGGCTCTTCCTTCTGTGCGTGTTCGGGAGGCTTACGTCTCG[C/A]CCGTGGTCCCTGGGTGGCC TGAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA</p>
stSG8064 a	23 G C ---				<p>AGCTGGCTCTTCCTTCTGTGCGT[G/C]TTCGGAGGCTTACGTCTCGCCGTGGCTCCCTGGGTGGCC TGAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA</p>
stSG8072	59 A G ---				<p>CACCATCATCACATCGAGTAGGCTGAGGAGCAGGAGGGGTGGGTCTTGTCTGTCTTAGGG[G/A]GTGGC AGAGGCAGAAAGGAAGTCCGAGTATTAGTGGCCGATGCGAGTTCAGGCTGTGCTGTTCAAAA</p>
stSG8100	40 A G ---				<p>ATACACCCACACACCCCACTCAACCTTGTATCAAAATCC[A/G]AAGTGTAACATAAAGTATAAGAAAT ATCATGACTAGTTAAAGATAGCAAATACCATAAGGTACAAAGTTCAAGTATTAGTATAACCAAGTAT CTGAGTAACAAATGTCTTGGAAATGGG</p>
stSG8102	138 T C ---				<p>AAGGCTCCTTTGAAAGCATGGTTTATTTGTCCATTAACTTGTTCCAGCTATACTGAAGTATGATT GACAAATAAACTTGCATATATTTGAGATGTACAGTGTGATGATACATGTATGTATACAAATGTGAAA TGA[T/C]JTGTCATAATCATAATCAATAATTGGTATATTGGTTTAGGAAATGTGATGGT</p>
stSG8105	110 A G ---				<p>CAGTGGTTCTCAAACCTCCAGCGTACACGAGGATGGTCTTGTCGTTGTTAATACACAGATGACTAGGCC CACCTGCGGAGTTCCTGTTGGAGTCTAGGCCCTAGAAATATTC[G/J]TTCTAACAAAGTTCCCAAGGTGA CCCTGAGGCTCTGGACTGGGAACATGCTTTGAG</p>
stSG8130 b	96 T C ---				<p>GTGTGTACATCATTTGGGAATGGAGGGAATAAATGACTGGATGGTGCCTGCTTTTTAAGTTTCAAATT GACATTCAGACAAGCGGTGCCTGAGCCTT[C/GT]GCCGTGCTTCAGATCTTCACAGCACAGTTCC</p>
stSG8130 a	36 C G ---				<p>GTGTGTACATCATTTGGGAATGGAGGGAATAAATGA[G/C]JTGAGTGGTGCCTGCTTTTTAAGTTTCA AAATTGACATTCAGACAAGCGGTGCCTGAGCCTGTGCTTCAGATCTTCACAGCACAGTTCC</p>
stSG8145 b	124 T A ---				<p>TTGTGGACTTCAAATCTTTCCCTCAGATTTTAAATGACATTTAATGATGTACATATTTTTAAAAATTT AGACACATTTTAGAGAACACAATTTGTAACACAAATCTAAGAAATGAATGAGATGTT[A/J]CTGAAA TCTGATTCAAACACTTATCTTAAACTGACTCTGTCAATCCCTCIGCTGTGGAAGG</p>

-291-

siSG8145 a	97	C T	---	---	---	TTGTGGACITCAAATCTTTCTTCAGATTTTAAATGACATTATGCGATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATTGTGA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACITATCTTAACTGACTTCTGTCAATCCTCTGCTGTGAAGG
siSG8150	36	A G	---	---	---	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAAATAGT[A/G]ATAAATAATAACGGGAATCCTAGGCAT TCGTGTTTCTCTATGTTTTAACAGGATTTTCTCTAAATGTTTCGCTATTAAATACCATGCAGGAAAT GGGAAAT
siSG8340	30	C T	---	---	---	AGAGGATTATGGAGAGAGCTGGGCAGGAT[C/T]CAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAGAAAAACGCTCATCAAAA
siSG8466	111	G A	---	---	---	TGTGATTGGGTGACTGTAGCCTAAGGATAAATGAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTAATTTGCACCTACC[T/G/A]TGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	--	--	---	---	---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCCCGTCTCCCTGCGTGGGGGCCAACCCCGCTTCCATGA GGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCCTGAACATCTGCACAAAATGGCCTGC
ESTD-ADA	--	--	---	---	---	ACCATCTTACTATGCGAGGTAAGTCCATACAGAAGGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGTCACCTGTTCTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCTCGGCACTGAGCTGCAGAOCC GCAGACCAACTCCTGAGCTTCTGGGCTCTGAGCTTGTCCTC
ESTD-AK- 168	--	--	---	---	---	GGGAGTGCAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTTCTCATGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	---	---	AATCCAGCATTTAGGAGGCTGAGGCAGGCATATCAACCAGGTCAGGAGTTTGAGACCATCTGA CCAAATGCTGTAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGTGCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGGCGAAGGTTGTTGAGCCCGAGAT GGCACCATTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTTC
ESTD- ANT1	--	--	---	---	---	TCTCTGTCAATTCCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGGCAATTAAACCAAGTAATTCA TGGACTGCCCAACTGCGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD- APOA2	--	--	---	---	---	CCAGGTGTTGTGGCACGTGCCTGTATCCAGCTACTCGGGAGACTGAGGCATGAGAAATCTTTTGAAC CGGGAGCGGAGGTTGCAGTGAGCTGACATCGGGCCTGCACTCCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD- APB8	--	--	---	---	---	GGAGAAATGGAGCCTGTGGGAAGGAGGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAGGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGTGCACACACTCATGAAGCT GGCCAGGGGACACCAATGGCACAAGCCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAGCCCATCCCCCAGAAATTGAGCTGCTGCATATATTGACCCAAAC

ESTD-AT3a	--	--	---	---		AGACCTCAGTTTCTCTTGTAAGGGAAGTTTGTCTTGATCTCCATGGCCCAGCCAGCACTG GTGCCCTGTGAGTCTGATCAGGTAGAGAGATGGACCAGGTGGAGGAAATTGTAAAAGGGCATTG GAATTCAGAGCAAGAGACAGATAATTAAGAGCTGGGGAATGTGG
ESTD-B9AR	--	--	---	---		GGCTGCAGGGGTTCGTGGGAGCGGCCCTAGCCGGGCCCTGCTGGCGTGGCGGTGCTGGCCACC GTGGAGGCAACTGCTGTTTCATCGTGCCATCGCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTGTTGACTTCGCTGGCGCAGCGCACCTGTTGATGGACTCCTGTTGGTGCGCCGCGCGCCACCTTT GGCC
ESTD-BA511	--	--	---	---		GGGCAACATAGTGAACCCCATCTCTACAAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCACTGCA
ESTD-BCL2	--	--	---	---		AGCTGGATTATAACTCTCTTCTCTGGGGCCGTGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAGGATGGCGACCTGGGAGAACAAGGTACGACAACCGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTCGAGAGGGGTACGAGTGGATCGGGAGATGTGG GGCGCGCCCCGGGGCGCGCCCCGACCGGGCATCTTCTCTCTOCCA
ESTD-BCR	--	--	---	---		CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCATCTGCGCAAGA GACCAAAGAGGTGAGCTTCTGTTGTCCCGGAAAGGAGCGAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA
ESTD-BRCA1a	--	--	---	---		AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGTTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	--	--	---	---		ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTAAAGAAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	--	---	---		ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAAATGACATTAAAGGAAGTTCTGCTGTTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTACCCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGGCCAAAGA AATTAGAGTCCTCAGAAGAGAACCTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	---	---		ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTAAATTTGCTCCGGGAAGACATTCATCAA CCCAGTCAGTTTGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCTTTCAACCATGCATTCCATCTAA GCTCTGCAAAAT

ESTD-C7	--	--	--	--	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAAATCCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	GGCAAGTTTTTATTGATAGAGAGGAATCAAATAATGGCAATGAGGAGACATCACTGGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCACCACTAGGGCGGATACAAAGAC AGGAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAG TAACATAATTGTCTTCAATTATGGTCTTTCCCGGCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	TAGAACCATCAAAGAGGAATAGGCTGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTTCCCGGCTTCTCTCACACATACAGAGCCCTTACCAGGACCAGACAGCT CTCAGAGCAACCCTAGCCCATACCTCTTCCCTTCCAGAGGACCTGAAACAGTGTCCCACCCCGA GGTGGCTGTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	--	--	--	--	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTGTTGAGCCATCAGAGGAGAGATCTCCACACCCCAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGACCCAGTGGAGCTGAGCTGGGTGAATGG GAAGGAGGTGCACAGTGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	GTTTTCTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTTCGCCGTG TCTGCTCTCGAACCCAGGCGATGGAGATCCACGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTTGTCACAGAGTCTTACCAAGCAAGGGTCTGTCTGCCCC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCCGTG
ESTD-CB27	--	--	--	--	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTTCGATTTCAGGAGTGTGTGGAGTCTGCTCATCACTGACCTATCTTCTGA TTTAGGGAAGCAGCATTCCTTGACATCTGAAGTGACAGCCCTCTTCTCTCCACCAATGCTGCT TTCTCCTGTTCACTCTGATGGAAGTCTCAACACCACTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	AGAAATGATATAGTCTCAAACCTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTGTCACCTTCAGGGTGTTCAGGGTGGAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACATACTGCCTTTG GTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	TGAGAGAACACCTAGTCTCCATCCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGCTGGGACCTGGAACACTGGACTCTTTCTACTGCAGCAGACAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATACTTTTATTTGACCAACACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	GCCGAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTAGAAGACATGTTTGATGCCCTAGAA GGCAATTCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCCTCCTCATCATGAAAC TGGGAGGCGGGCATAGTCTCATGCTGTATGCCGCTGTATCCAGCATTTTGAGAGGCTGAGGCGGTGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCAACAT

ESTD- CTLA-4	--	--	---	---	---	ATGGCTGGCCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTACAGGAACCTGGCCCTGCAC TCTCTGTTTTTCTCTCTTCATCCCTGCTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
ESTD- CYP2D6	--	--	---	---	---	CAGGCCAGCGTGGTGAGGTGGTCAACCATCCCGGCAGAGAACAGGTTCAGCCACCACCTATGCACAGGT TCTCATATTGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	---	---	---	AAAAAACATTTTAAACACCTTTTCAATCATATACACCATAAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAAATTAATTGCAATCTAAATGTCAATGTAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAATATTACATATCTGGATTAAATATTGCCCCATAT CTGCATGTC
ESTD- D17S33	--	--	---	---	---	CATCCCCAAGCCCATCCTTAGCCACTGGCATTTTTTCCGCCCTCTGACAGATACACTCAGGGCCCGT CATGCTGCACACATCCAGGGGGCGCCCTACCCCTTTGTAGTCCATGGGAAAGCCTCCTCTGGGGCGGTG GGTTGTGTGGCTATGTGGTGTCTGTGTAGACGGGGCTTTGGTTTCAGTTGCACTATTGCGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCCTC
ESTD- D18S8	--	--	---	---	---	TTTGAGACCACCCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGGTACATGCTATCGTAATCCAGCTACATCGGGAGCTGAGCGAGGAGATTGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCCAAGATCACACCCTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	---	---	---	AACTGATTAGAACCTGAAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCCAATAAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTTGT TTATCAAACCTATTTATCACTATTTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	---	---	---	AGGTTCCACATTATTGCTGATGTTTGGTATGTTTCCAGGAGCCTTGATGTCATCTGTATCTCTCAG GTATCCACCTTGAGACGTACTTTTCAAAGCTCTCTACAGCCGTTGTGTATTAAATTCAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAATATGGTCAGGTTACAGCTGATTCCTC AGAGTGAACATACCTGCTCCTAGAAAGCCAGAGTCATCTGGAATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATACTGTCTCTTATTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAAATGTATTT CTTAAACAAATAAACTTGAAGTCCAAAATTTACTCCTTGATCCATGGACTGCAGAAATAATGTTATTT TAGCTGTCAGAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATATTTTGAGAGGAATCTGTTTTCATGTCAGTAG
ESTD- D4S95	--	--	---	---	---	CTTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTTGAGAAGAGCAAAACAACCTTCAAGG ATAATGGGGCAATCACTTTCCTTCTCTTTAGAGTCTACCGG

ESTD-D7S399	--	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGATAACTGCTAGAGACCCAGTCTCTACATCATCTCTTACAAAACATTTTCATCCATGGAAGTCCATACTAGATAATTTGAAGAAACAAACATGACAAAACATTTTC
ESTD-DM	--	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGTTGCACGTGTGGCTCAAGCAGCTGCTCGGCTCCACTTCATGGGTGTGGGCGCTGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGGAGACA
ESTD-DRD1	--	--	---	---	---	GAATGCTGATTATCTGTGTGAGAACCAACTTCTGGCCTGTGGTAGGGGAGCTGCTTCCAAGACCCTCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DRD2	--	--	---	---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCACACAAACGGTCAGCACCCAACTGAACCTGCGAGATGAATCTCTGCCACACATGCTCATCCCCAAAAGCTAGAGGAGATTGCTCTGGGGCTGCTATTAAAGAACTAAGGTAC
ESTD-DRD3	--	--	---	---	---	TCTGCTTTGGTGCAGGAGGCTGCCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA
ESTD-DRD4	--	--	---	---	---	GCCCAACCGAGAGACCCGGTACAGCCCATCCACCCAGCCACCAAGCTGACTCTCCCGGACCCG
ESTD-DRD5	--	--	---	---	---	TCCACACGGTCTCCACAGCACTCCGACAGCCCGCCAAACAGAGAAGAAATGGGCATGCCAAAGACACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD6	--	--	---	---	---	AAGACGATGGCCAGGATGAGCGCGAGTAGGAGGGCATAGTAGGCATGTGGCGGGCGCTGGCTGG
ESTD-DRD7	--	--	---	---	---	CACCTGTGGAGTTCTTGCCCCACAGGTGTAGTTAGGTGGCCACTCAGCTGGCTCAGAGATGCCATAGGCCAGAGGAGTGCGTATGCCAAGGGGCTTCTGTGAGGAGA
ESTD-DRD8	--	--	---	---	---	TCTTTAGGATCCGCATCTGCGCTGGTTGGGCATCGCTCGCTAGGTGTACGCGGCTCCACAGCTGGGGTAGGGGGGTGTGCGCGGGCGGGTGCAGACCCACGCGGGCTGGGAGGACTTCAOCC
ESTD-DRD9	--	--	---	---	---	CGCTCACTCCGTTTCTGCAGCAGTCTCCGATCGTGACT
ESTD-DRD10	--	--	---	---	---	ACTCACAGTCTTTTAAGTGAAATGGTCGAGAAAAGAGCCAGGAGCCGTCCTGGCGCTGGCA
ESTD-DRD11	--	--	---	---	---	GTCCGTGGACGGGATGGTCTGGCTGTTTGAGATCTCAAAGGAGCGAGCATGTCGTGGACACACAGAGACTATTTTAGATTTCTTTTGCCCTTTGCAACCGAGAACAGCAATGCAAAAACCTTTTGAGAGG
ESTD-DRD12	--	--	---	---	---	GTAGAGGGGTGGGAAGGAACAAACCATGTCATTTTCAAGATTAGTTTG
ESTD-DRD13	--	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCTGCACCAATGGCTCCAAAGGCCGTAGGGAACTGGGGGATCTAGGGGATGGGTAGGAAATGGCCAGCCAGTCCCGCGGTGCTGGTGCCCAACAGAGGAGGCGGTGGAGGAGACAGGAGATGGGCTGGATGAG
ESTD-DRD14	--	--	---	---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCATGCTCCATTTGAGTTAATTTGTGTAAGTATGATGTTTAAGTCAAACCTCAATTTTTTTTTTCCATAGGTATGCCAATTTATCCAGCACAAATTTGTTTAAACCAAAAAAC

ESTD- G0DH	--	--	--	---	---	---	CGCAGACCGGTCAAGTGTGGGGTCGGGAGTGTGGAGGGAAGGAGGAGGAACTGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGACAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAGGGACCTCTGGTCGACCGTGTCTGCTGCCCCGTTTACAGCTGTCTGCTGCCGACAGTCGA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	--	--	--	---	---	---	GTTTATGATGGCAGCTCTAATGACAGGATGGTACGCCCTGCTGAGGCCACTCCTGGTCAACATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCOCCACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGCCCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCCAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACCACAGGCATATTG AAACCAAGTTTCCGTCAAAGACTTGAATTTACAGGTAAAGTGCATGGTTCCCTAGG
ESTD- GPPK2L	--	--	--	---	---	---	AGTCTTCATCTGGGGTGTCCAGGTAGATCCCTTTACCCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	---	---	---	CTGGGCTGCCCCGACGAGCTGCTGGCACCTGGACGGCGCGCCAGGCTACCTCTATAGTGGGTG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	---	TTGGAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGCCCTGGGCCACATCTGGCCTTG AGGGCCTGCAAGACCCCAAGAAAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCTCACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTTCCTTATCCCTGATGATTGGATTGGCTTCCCTGCTG
ESTD-HT2	--	--	--	---	---	---	GGGCTAAAATTTCCGAGCAACTTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGAGAAATAAAGGATAACCTGGGTTTCTGTGC TTTGCTTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	---	ACCAACGAGCGCGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAAGTGGTTCTTGGTGCTTCTATCGGCAAGAAATCGTACTTATTTGAATAGTAGAGGTAA ACCACAGCCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	---	AACACAAAGCCCCAGCAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGAGCCCTCGTCTGCTGTTGGTTTTCTTCCTTTCATCTTAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAGTAAATCCAGGATATTCTCCTACAAAATGA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	---	ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGAAGATGTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATCTCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCTACATTTGTGTGAGTGACGGGAGTGGTGATCCGAGAGTGTGGTGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACGTGAAAGT ATGTAATAACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATATCAATTATTATTATTATTTATTTTTTG AGATGGAGTCTGGCTCTGTACOCAGGCTGGAGTGCAGTGCACAAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCTCTGCTCAGCTCAGCTCCGAGTAGCTGGGAATACAGGCAACCCGCACT GTTCCCGGCTAAATTTTGTATTTTGTAGTAGAGACGGAGTTCCACCGT
ESTD-IL1B	--	--	--	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTACCTTGGGTGCTGTTCTCTGCTCAGGAGCTCTGTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAAATGCATTTAAAGTAACCTGCTAAGGTTTTTCCATTAAACCACCTATTACTTTAAAG AGAACTGTACATGACAAAATATTGCCATTACATGAGATCAACTATGAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGCTTTAAGAGAGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATTTCAAAATTGTAACCGTAGCAAAACGCAATGGTATTTAGA AAAAATAAAAAATTTCCAATATGATGCTGTGTATACCTGCTGCTGCCATGCAGCATCATAGCCTGT GGGAACCAAGGAGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTTCCTTACCATTCACTGAAAACGCACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCCAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGCACCTCACCACTCCAGCTTCTCAGCTCTGGCTGCTGCTGCTGCTGCA AGGGTTTGCTTAATCTCAATTCATGCTCTTTCATCTTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCGTGTTTTGCTTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTTATAAAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCTGCCCTCCAGCTCTGTCCCTAGCCGAACCTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAGCAGTAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTTCCAAGGGTTTGGCTAAGTTGCTGATTACCCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGTTCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAACTATACCAGATCCACAGACTGATATGGCTGGT

ESTD-NFKB1	--	--	---	---	AACATGGACTTGTATATTTGTACAAAAAAGGTTTTATTTCTAAAAAAGAAAAAGAAAA AAATTTAAGGGTGACTTATATCCACACTGCACACTGCCTAGCCCCAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATCTGAG AAACCTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD-NPPA	--	--	---	---	TGTCCTAGGCCAGCCCTGCTTGTCTCCTCCCTGGCTGTATCTTCAGTACTGCAAAAGAACACAGAC AT
ESTD-NRAMP	--	--	---	---	GGAGCAGGAGGTGGGAGGGGTCTGTCTCTCCAGGTCCACAGACCAGAGAAGCGCCTCAGTG TATCCCCACCCCCAATGTGGCGCTGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-NRAS	--	--	---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTTCTTTATGTAGGGTGATATTGGATACTTTTGTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTTGC ATTCCTGTGGTTTTTAAATAAAT
ESTD-OTC	--	--	---	---	GTGACCTTCTCACTTTAAAAAATTTACCGGAGAAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGAGGTAIGTAACA
ESTD-PAI1	--	--	---	---	GCCACCACCCACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGGCC TCAGGGGCACAGAGAGTGCTGGACACGTGGGAGTCAGCCGTGTATCATCGGAGGCGCGGGCAC ATGGCAGGGATGAGGGAAGACCAAGAGTCCTCTGTTGGGCCCAAGTCTTAGACAGACAAAAAOCCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	---	---	CTCTTCAGAACCCAGCTCTTACCAACACGACTTATGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACITTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTAAGCTTTCACCTAGGCTTCTGTATACCCATGCC
ESTD-PBDA	--	--	---	---	CCTTCTCATGCCAGATGGAAATTCAGTCCCTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAATCTCTACCCGACGTTGCTCGCATACAGACG GACAGTGTGGTGCAACATTGAAAGCCTCGTACC
ESTD-PS-1	--	--	---	---	GGGAGTAAACTTGGATTGGAGATTTCATTTCTACAGTGTCTGGTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCATAGCCTATTTCTAGCCATATTTCTAGCCATATTAATTGGTTGTGCCCTACATT ATTACTCCTTGCCATTTTCAAGAAAGCATTTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT CTACTTTGCCACAGATTATCTTGTA
ESTD-PXMP1	--	--	---	---	ATGAAACATGGTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTCTCTTTTTTTA ATGCAGAAAAGGGGAAAAAAGCGGAGCTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAGTCTTAIGAAATTAATCTT
ESTD-Per/RDS	--	--	---	---	ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG CTGGAGAAGAGCGTCCCGGAGACCTTGAAGGCT

-299-

ESTD-RDS	--	--	--	---	---	CCCGAGGAATCTGAGACGAGAGCGAGGGCTGGCTGCTGGAGAGAGCGGTGCCGGGAGACCTGGAAGG CCTTTCCTGGAGAGTGTGAAGAGCTGGGCAAGGGCAACAGGTGAAGCCGAGGGCGCAGACGCAGG CCAGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	CTTCGTGACGGGAGGTACGTCCTCCGCCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCC CTGCTGACAGTATGACCGCGCAGACTTGTCTACTATGAGAGGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGAGCCACCTGCCGTGGGGCCAGCCACT CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCAOCCGAGG
ESTD- SPTB	--	--	--	---	---	TGAACACCTGTGGTCCGGAGCCAGGTGTGTTCTCCTGGGAGCCTGAGGAGTTGTTGTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCCTGGACATACACCTTACCTCCTTTGGCCCGGAGAAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTGTGCACACCTCTGTGAAGACCCCAACCCCTGCCCTCC CCACCCCAAGCCAGTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	TTCACCTTTGTGGATTGTTCTTTTGTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCCTGTGCTGTGGGATATTGAAGAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTAAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCATTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACCTTTCTCCAGTATGGATGGGATATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	--	--	--	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTGAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAGACCCCCCTCAGATCGAGACGAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCCAACTTTCCAAATCCCCCGCCCGCGATGG
ESTD-TYR	--	--	--	---	---	TAGTGAAGTTTTCATCTCCTGTGACGTTCTGGATTCTTGTTCACCCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGCTCTCCAGATTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATTGATGTGCGTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCTATGGGGATGACA

[illegible]

-301-

EST11458 6	--	--	--	---	---	CCACITTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCACAGTGCTCATCTTGTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGACCTGTGCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAAAAACATTCTATGAGCCAGGAGAAAGATACGTATTCTGCAAGCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGTCTTCCCTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCAGATGCATCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCCTGTTTCCAGTGTAAAGGCATGCANAAAGCCTCCACAGGCTGCTATAAT ACAGGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTTGGCATTGCCGCOCTCTCTGGGGCCCGTGG TCCTCTGGTGTGCTGGGTAGTCTGAGTCAACGGTGTCTCTAGTGAAGCTGGTCTGATGGCAACC CTGGGAACGATGGTCCCCCAGGTCGGATGGTCAACCCGGACACAAGGGAGAGCGCGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCAAAGGAAATGGCTACCCAACTGCCTTCATGGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACTTACCACCTGCAAGAACAGCATTGCATACATGATGAGGAGACTGGAACCTGAAAAAGG CTGTCACTTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGAGGTTCACTTACACT GTTCTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCCTTCCAAATAGAGCCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTACTCCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST44438 7	--	--	--	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCGGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCCCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAAGG CCATTGGCTATCTCAACACTGGTGGTGTGATTTACTTGAGTAAGGAAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACCTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTTAGCGTGGTCTGATGTTGCTACTA TAGTCCAAAGTGAA

EST10398 2	--	--	--	--	---	---	TGCCTGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGGGGCCATGGTA AGATGCTGCCACCTCTATCTACTTGATGATGTTTCACATTGGGGCTTGACTTTCCAAACACGGAGAAG CATTGTTTCTTCGGGCCAAGAAGGTATCTACCAATAGTGCTATTAGGCAATTG
EST36751 7	--	--	--	--	---	---	CCAAAGTCGTTCAATTTAGCTTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTCTGATCTATGGTTCAAGTTAAACAG
EST40562	--	--	--	--	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTCTGCCCAAACCTTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCATTAATAACAAATATTTACCTTTTGAAAAATAAATG AAGGATTGACCTGCTTCGCTCTGGAAGAGTATCCGTCCTGACGTTTGAACAATAACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	--	--	--	--	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGACGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTTCAACACCTACGTCCACTTCCAAGTAAGGCAAACTCTCTGCTGCTGCTGGC CCTAGGACTTAGTATOC
EST70523 3	--	--	--	--	---	---	TTCCCGCAGCCCCCATCTTGGCACCTTGGTCCCTCAGGGGCCACCCCGCGGCACTCACCCGCTCT CGCTCTGGTAACATCCGGCCGGCGCGCTCTTGACACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCCGTCCCGGGCTTCCAGGGGCCAGCCCTGCAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707 7	--	--	--	--	---	---	CAGTGATCTGGAAGCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGCTTT AAGTTCAAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGACCTAGAAATACACGAGACCGA ATGTATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTGTGGTAGGCCAGGTTTATAGCA CACTTGTACCTACATTTCTGATTGGTGGACTCTTGTGCTAAGAACCTT
EST74167 6	--	--	--	--	---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACTGACCCCGGTGGCGGAGG AGACGGGGCAGGGCTGTCCAGGAGCTGCAGGGCGGCGAGCCCGGCTGGCGCGGACATGGAGGA CGTGGCGGGCGCTGGTGAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGACCGGAGGAGC TGCGGGTGGCTCGCTCCACCTGGCAAGCTGGTAAGCGGCTCCTC
EST43211 8	--	--	--	--	---	---	CGCCTGGTGAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGGGTGGG CCTCGCTCCCACTGGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAGCGCC TGGCAGGTACAGGCGGGCGCGAGGGCGCGAGCGCGCTCAGCGCATCCGCGAGCGGCTG GGGCCCCCTGGTGGAAACAGGCGCGCTGGGGCGCGCAGCTGGGGCTC
EST36770 4	--	--	--	--	---	---	TGTAGCCAAAGTCACCTGCATCATCTATTGGTGTCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAT TCAACCCCTCCGATAGGCTGGGCTGACCAAAAATATACTGGTTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTATACCTTATTGGAAGGCCCTAAAGAAGGCTTATG

EST26021 1	--	--	--	---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACCTACCAATGA GCATTAGCTACTTTTTCAGAAATGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCCITTTTGCAACAAGACAAAGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCCAATAAGCTTCTGGTTCTACTTCTCTCTCCACAAGCCCAATTCACITTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTCCGAATCCTCCTCCTGAAAGTGGCCGGTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGGTCTCTCGTGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGAGTGGGTTTAGGACGCGGGTCTCTCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCCAGGTACACATTCCAGAAGAGGAGGGTGGTCACTGAGCCTGGGTAGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTCCTATGGGATTGACTTTATTTTCTCCATTGCTTACCTTTACAGGTGTTAATAGTGAAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAACATTTGAAGTTGTTTTGAAGTGGTGACCTTTAATACAACCTAG CAGACGGAAGTGAAGTCAAGGTAAGAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCACACAAGAGACCGGCTCAAGG ATCCAAAGGCCCAACTCCCGAACCACTCAGGGTCCCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCCCTCTTTCTCTCCCTTGGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCCAGCAAGAGAAAAGAGACCCCAAGAAAT CACAGGTGGGCACGTGCGCTACCGCCATCTCCCTTCACGGGAATTTTCAGGGTAAACT
EST74082	--	--	--	---	---	TCCAGGTGGCTGGACCCCAAGGCCCCAGCTCTGCAGCAGGGAGGACGTGGCTGGGCTCGTGAAGCATG TGGGGTGAGCCAGGGGCCCAAGGCAGGGCACCTGGCCTTACGCTGCCTCAGCCCTGCTGCTGTCAC CCAGATCACTGCTCTTCTGCCATGGCCCTGTGGATGGCCTCTGCCCTGCTGGCGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGGC
EST45311 0	--	--	--	---	---	GCCCTCCTCTCTTCCAATTCTGCCCTATAGTTTCTCTATTAAAGTGAACATACATGCATTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTCAATTAACAGCCCTTATTCAATGGCCCTTTTCTTTTCAGTAGTA CATACACATCTGTGTCATTTGTTGAAT

EST65258 8	---	---	---	---	TGCCCCATCAGCGGCGGAGACATGGCTTGCCACAGCTTTGAGGATGTCACCAATTAAACAGAAAT CCAGTTATTTCCACCCTCAAAATGACGCCATGGCGGCGGGTGCTCTGGGGCTCGTCGGGGG ACAGCTCCACTCTGACTGGACAGCTTTTGCAATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTCTGTCGCAAGTCAGGACATCAGCTGATTAAA
EST38216 3	---	---	---	---	ATCAGGATGAAGTGGACAGGAGGAGAGGGCCAACTGTCTATCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 --	---	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATAGCAATTTGTTTAGCATTACCTAA TTTTTCTCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAG TTTTTTTCTCGAAGTGCCAGTATCCAGAGTTTGTTTTTGAACCTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTTGGGTTTTTGGTGCATGCA
EST35879 9	---	---	---	---	GAGATCGGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGCGTTCCACCGATG GAACTCGCGGCAATCTCTGACACGTGTGCAACCGGCTGTACCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCTGGATGAA
EST68308 5	---	---	---	---	GGAAAGAGATTTAAGAAGCTTGATTGGACAATCTCTGGTTCTTGAGTGTGGAAGAGTTTCATGCTCT GCCTGAGTTACACAGAAATCCTTTAGTACAGCAGTAATAGATATATTCACACAGATGGGAATGGA GAAGTAGACTTTAAAGTAAAGTAGTATATTTTTTA
EST54045 6	---	---	---	---	GGAAATTTAAAATATTTTAAATACCTCCATTTTGCTTATCTCTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTATGATGTCATGTGGCAATTTGTTTCTTACAAAATCGGATGGAAATCT GTTAAGTAAGTACTGTTTGGCTTGGAAATTTGATTTTAAATGTTGACTTTATCAT
EST52908 0	---	---	---	---	ATCACAGGTCTCTGGTCTCTGCGCATCTTTCCTGGGAGAGATGGTGGTCTGCAAGCCCTTTGG CAATGTGAGATTTGATG
EST19590 --	---	---	---	---	AGGAGAAGCTGAGGAGGGGGAAGAGAGACAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAAATGAC
EST76136 --	---	---	---	---	TGAAGCTTCTGCCAGCTTGCAATTTCTAGGAGAACCCGCTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0	---	---	---	---	CTCTGGATGGGTTACAGGTGGCAGGCCACAGCCAGTCCATCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGAGAACAGGACAGCACATGGCGGGATGGCCGGGGAGTTCTGGT TGCGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTTGOGATGCCTAAACCTTTGTTCT TGCCAAAGGAGGGGGGTGCCATGCCTGAGATGTAGATGGGCC
					Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

-305-

EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

-306-

CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

-307-

12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

-308-

20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
- 5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.

INTERNATIONAL SEARCH REPORT

International Application No

PLI/US 97/20313

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/68 C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 12607 A (MOLECULAR TOOL INC) 11 May 1995 see the whole document	1-20
X	WANG D ET AL: "TOWARD A THIRD GENERATION GENETIC MAP OF THE HUMAN GENOME BASED ON BI-ALLELIC POLYMORPHISMS" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 59, no. 4, October 1996, page A03 XP002050641 see abstract	1-20

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

23. 09. 1998

Name and mailing address of the ISA

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Authorized officer

Knehr, M

INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL10 emb1 Accession number: hst27766, 12 January 1995 ADAMS M D ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence" XP002067789 * Sequence *</p>	1-3,10, 11
X	<p>SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS, USING PCR AND SOLID-PHASE MINISEQUENCING" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 52, no. 1, January 1993, pages 46-59, XP002050638 see abstract see page 47, column 1, paragraph 3 - page 50, column 1, paragraph 1 see page 51, column 1, paragraph 3; figure 1; table 1</p>	1-3, 7-10,13, 14,17-20
X	<p>FR 2 722 295 A (ROUSSY INST GUSTAVE) 12 January 1996 see abstract see page 1, line 5 - page 2, line 17 see page 9, line 9 - page 10, line 15; tables 2,3</p>	1-3,7-9, 17-20
X	<p>HRUBAN R H ET AL: "K-RAS ONCOGENE ACTIVATION IN ADENOCARCINOMA OF THE HUMAN PANCREAS A STUDY OF 82 CARCINOMAS USING A COMBINATION OF MUTANT-ENRICHED POLYMERASE CHAIN REACTION ANALYSIS AND ALLELE-SPECIFIC OLIGONUCLEOTIDE HYBRIDIZATION" AMERICAN JOURNAL OF PATHOLOGY, vol. 143, no. 2, 1 August 1993, pages 545-554, XP000572114 see the whole document</p>	10-16, 18-20
X	<p>GROMPE M: "THE RAPID DETECTION OF UNKNOWN MUTATIONS IN NUCLEIC ACIDS" NATURE GENETICS, vol. 5, no. 2, October 1993, pages 111-117, XP000615290 see the whole document</p>	18-20

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INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 97/20313

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>NIKIFOROV T T ET AL: "GENETIC BIT ANALYSIS: A SOLID PHASE METHOD FOR TYPING SINGLE NUCLEOTIDE POLYMORPHISMS" NUCLEIC ACIDS RESEARCH, vol. 22, no. 20, October 1994, pages 4167-4175, XP002015765 see the whole document -----</p>	18-20

INTERNATIONAL SEARCH REPORT

I. national application No.
PCT/US 97/20313

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-20 (partially)

INVENTION 1: An isolated nucleic acid segment including a polymorphic site having the nucleotide sequence of SEQ ID NO:1149, or the complement of that segment or portions thereof, an allele-specific oligonucleotide probe or primer hybridizing to such a segment or its complement, and a method of analyzing such a nucleic acid by determining the bases occupying the polymorphic site(s).

2. Claims: 1-20 (partially)

INVENTION 2 to INVENTION 2669:

-Idem as invention 1 but limited to the sequences having SEQ ID Nos. 1150 to 3817. (Invention 2 is limited to SEQ ID NO:1150, invention 3 is limited to SEQ ID NO:1151, ..., invention 2269 is limited to SEQ ID NO:3817).

For the sake of conciseness, the first group is explicitly defined, the other groups are defined by analogy hereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC/US 97/20313

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9512607 A	11-05-95	AU 8132194 A CA 2175695 A EP 0726905 A US 5762876 A	23-05-95 11-05-95 21-08-96 09-06-98
FR 2722295 A	12-01-96	NONE	